32, Appī 7231, Ap 6406, Ap 7169, Ap 7411, Ap 13778, A 4879, Ap 4, Appli

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923, App 2874, Ap 3137, Ap 4004, Ap

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32168, 75 24, Appl 3057, Ap 105, App 111, Appl 377, Ap 4316, Ap 14, Appl 10, Appl 10, Appl 10, Appl 10, Appl 10, Appl 10, Appl 201, Appl 377, Appl 10, Appl 377, Appl 37

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US-09-134-001C-3137

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US-09-634-955B-32

US-09-634-955B-32

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17923, A
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Sequence 8, Appli
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                                                                         September 16, 2004, 07:44:20 ; Search time 18 Seconds (without alignments) 108.988 Million cell updates/sec
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29293, A
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    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-328-452-376
US-09-198-452A-376
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US-09-134-0011-3241
US-09-134-0011-3241
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US-09-58-252-991A-2601
US-09-58-252-991A-2601
US-09-252-991A-29293
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Maximum Match 100%
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Match 1
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Sequence 13474, A Sequence 5237, Ap Sequence 5104, A Sequence 11014, A Sequence 6726, Ap Sequence 10777, A Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

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Sequence 3 Sequence 3 Sequence 3 Sequence 9

Sequence 9, Sequence 9, Sequence 8,

Sequence 8

Sequence 8, Appl Sequence 7503, ? Sequence 13595,

Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 25, Appl Sequence 18, Appl Sequence 18, Appl Sequence 17, Appl Sequence 17, Appl Sequence 440, App Sequence 7202, Ap Sequence 440, Appl Sequence 440, Appl Sequence 44, Appli

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TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea mays
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US-09-328-352-8139
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US-09-328-352-7407
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Sequence 8, Application US/09364230
Sequence 8. Sequence 8. Applicant Normation:
APPLICANT: Cahoon, Rebecca E. APPLICANT: Kince, William D. APPLICANT: Kincey, Anthony J. APPLICANT: Kincey, Anthony J. APPLICANT: Rafalski, J. Antoni
TITLE OF INNENTION: BL2ymes Involved in Degradation of Branched-Chain Amino Acids
TILE REFERENCE: BB-1178
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT APPLICATION NUMBER: G0/094,990
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
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Sequence 7.2. Application US/10164595

Patent No. 6657054

GENERAL INFORMATION:
APPLICAMTON: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1

CURRENT PILING DATE: 2002-06-10

NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7.2
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Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.0%; Score 166; DB 4; Length 547; 100.0%; Pred. No. 2.3e-15; ive 0; Mismatches 0; Indels
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                                                               ALIGNMENTS
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; Sequence 4, Application US/09364230
; Patent No. 634839
; GENERAL INFORMATION:
   APPLICANT: Cahoon, William D.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni
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ilarity 64.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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US-09-364-230-8
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Sequence 8139. Application US/09328352

Fatent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 8139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7407, Application US/09328352
Sequence 7407, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
RAPPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 299
LENGTH: 299
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Best Local Similarity 52.8%; Pred. No. 1.5e-06;
Matches 19; Conservative 5; Mismatches 12; Indels
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FILE REFERENCE: BB-1178
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
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US-09-328-352-8139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.9
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                             21; Conservative
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CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gary Br
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US-09-198-452A-376
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US-09-198-452A-376
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                                                                                                                                                                SEQ ID NO 24727
LENGTH: 295
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                      Sequence 5109, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A DOUCETTE-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
BNTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CURRENT APPLICATION DATA:
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION UNDRER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAMME: ATINICALION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
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LOCATION: (B) LOCATION 1...299
US-09-107-532A-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 299 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                              CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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Best Local Similarity 52.9°
Marches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02354
                                                                                                        US-09-107-532A-5109
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                                                                                  RESULT 6
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GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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     Score 98; DB 4; Length 295;
Pred. No. 4.9e-06;
7; Mismatches 9; Indels
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42.5%; Score 85; DB 4; Length 204
Best Local Similarity 42.1%; Pred. No. 0.00022;
Matches 16; Conservative 10; Mismatches 12; Indels
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63.0%; Pred. No. 0.0005;
live 1; Mismatches 9; Indels
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                                                                                                               1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                              Query Match
49.0%; Score 98; DB
Best Local Similarity 52.9%; Pred. No. 4.9e
Matches 18; Conservative 7; Mismatches
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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Patent No. 6559294
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Best Local Similarity 63.09
Matches 17; Conservative
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; sequence 17923, Application US/09252991A; sequence 17923, Application US/09252991A; patent No. 6551795; Patent No. 6551795; GENERAL INFORMATION:

| APPLICATION: MICHEL ALI MICHEL ALI AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; TITLE OF INVENTION NUMBER: US 60/074,788

| PRIOR FILING DATE: 1998-02-18
| PRIOR PILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| SEQ ID NO 17923
| LENGTH: 330
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GENERAL INFORMATION:

APPLICANT: LYND DOUGETEE-Stamm et al

APPLICANT: LYND DOUGETE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: DEPLEMBLE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22003, Application US/09252991A

Sequence 22003, Application US/09252991A

Sequence 22003, Application US/09252991A

Barbicon Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FULE REPERENCE: 107196.136

PRIOR RAPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR PAPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

SEQ ID NO 22203

LENGTH: 221
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37.5%; Score 75; DB 4; Length 221
Best Local Similarity 57.7%; Pred. No. 0.0065;
Matches 15; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Indels
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38.5%; Score 77; DB 4;
Best Local Similarity 47.1%; Pred. No. 0.0054;
Matches 16; Conservative 5; Mismatches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 FAGLGLMGVPMCRRLLAAGYPLAVWNRSPGKREL 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-22003
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US-09-134-001C-3241
US-09-252-991A-17923
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
CURRENT APPLICATION NUMBER: US/09/364,230
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
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40.2%; Score 80.5; DB 4; Length 307;
Best Local Similarity 31.0%; Pred. No. 0.0016;
Matches 18; Conservative 10; Mismatches 9; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
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Best Local Similarity 71.4%; Pred. No. 0.001;
Matches 15; Conservative 1; Mismatches
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              LGLGLMGSGIVSNLLKMGHTVTVWNRT 29
                                                          ; Sequence 9294, Application US/09489039A; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 SNLLKMGHTVTVWNRTAEKCD 34
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                                                                                                                                                                                                             Sequence 2, Application US/09364230 Patent No. 6348339
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US-09-489-039A-9294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Microsoft Office 97
SEQ ID NO 2
LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: UNSURE LOCATION: (247)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-09-489-039A-9294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (244)
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :|::||: |:||: |:||:||: ||: || 7 GVVGMAVMGRNIALNIESRGYTVAIYNRSKEKTE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: 6-phosphogluconate dehydr
TITLE OF INVENTION: ogenase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows 95
SOFTWARE: FRSTENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/584,628
                                                                                                                                              GM10140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GM10140
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APPLICATION NUMBER: 09/058,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09584628 Patent No. 6309866
                                                                                                                          36,795
                                                                                                                                          REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                    | LENGTH: 474 amino acids
| TYPE: amino acid
| STRANDEDNESS: single
| TOPOLOGY: linear
| US-09-058-692-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             474 amino acids
                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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US-09-584-628-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 37.0%; Score 74; DB 4; Length 490; Similarity 38.2%; Pred. No. 0.023; 13; Conservative 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09058692
Patent No. 6162618
Patent No. 6162618
GENERALI INFORMATION:
TITLE OF INVENTION: 6-phosphogluconate dehydr
TITLE OF INVENTION: 0genase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
PILLING DATE: US/09/058,692
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 3241
LENGTH: 474
                                                                                                                          TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
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STATE: PA
COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
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Matches 13; Conserv
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: BB-1178
CURRENT FRILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER APPLICATION NUMBER: 60/094,990
SUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 12.
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                                                                                                                                                                                                                                                                                                     Score 68; DB 4; Length 74;
Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                Indels
                                APPLICANT: Jobert, S.
APPLICANT: Gordano, J.Y.
ITLE CONTRIBUTION: ESTS and Encoded Human Proteins.
TILE REPRENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 6407
LENGTH: 74
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
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Pred. No. (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-364-230-12; Sequence 12, Application US/09364230; Patent No. 6348339; GENERAL INFORMATION:
              APPLICANT: Dumas Milne Edwards, J.B.
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52.0%;
                                                                                                                                                                                                                                                                                                             34.0%;
ilarity 37.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-621-976-6407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , LOCATION: (184)..(201)
US-09-364-230-12
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Best Local Similarity
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Matches 13; Conserv
GENERAL INFORMATION:
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LOCATION: (
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APPLICANT:
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Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICANTON NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PEPLICANTON NUMBER: US 60/128,706
PRIOR PEPLICAND DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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GENERAL INFORMATION:
GENERAL INFORMATION:
THILE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ABREGIONOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26001
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  36.5%; Score 73; DB 4; Length 474; 35.3%; Pred. No. 0.031; Live 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 486,
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                    0.031;
..hes 12; Indels
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36.0%; Score 72; DB 4;
Best Local Similarity 34.4%; Pred. No. 0.044;
Matches 11; Conservative 12; Mismatches
                                                                                                        1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.5%; Score 69; DB 4; ilarity 45.2%; Pred. No. 0.072; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 GVVGMAVMGRNLALNIESRGYTVSIXNRSSDK 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6407, Application US/09621976 Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT;
ORGANISM: Proteus mirabilis
US-09-543-681A-5380
        36.5%
Query Match
Best Local Similarity 35.3%
Matches 12; Conservative
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es 14; Conserv
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US-09-252-991A-26001
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US-09-543-681A-5380
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Best Local &
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Sequence 27650, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PILIDING DATE: 1099-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142'
SEQ ID NOS: 33142'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELATING TO KLEBSIELLA
                                                                                                                                                                               Gaps
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APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATITIES OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATITIES OF INVENTION: PREUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747
                                                                                                                                   DB 4; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 543;
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                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                          8; Mismatches
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                                                                                                                                 Score 65;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.0%; Score 64; 48.0%; Pred. No. (
                                                                                                                                                                                                                                             2 FLGLGLMGSGIVSNLLKMGHTVTVWN 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12581, Application US/09489039A Patent No. 6610836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GLGLMGSGIVSNLLKMGHTVTVWNR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 GFIGTGIMGKPMAQNLQKAGHSL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GFLGLGLMGSGIVSNLLKMGHTV 23
                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Klebsiella pneumoniae
                                                                                                                              32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.5%;
                                                                                                       Query Match
Best Local Similarity 46.27
Best Local 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                US-09-252-991A-29293
                                                                                                                                                                                                                                                                                                                           RESULT 25
US-09-252-991A-27650
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US-09-252-991A-27650
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US-09-489-039A-12581
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LENGTH: 303
                  LENGTH: 154
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APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREI
THE REPERENCE: ELITRA.008A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR PILING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FactSEQ for Windows Version 4.0
SEQ ID NO 438
LENGTH: 292
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR SEQ ID NOS: 33142
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REPERENCE: BB-1178
CURRENT APPLICATION NUMBER: US/09/364,230
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER APPLICATION NUMBER: 60/094,900
EARLIER PILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
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Pred. No. 0.12;
6; Mismatches 7; Indels
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0.21;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTV 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-364-230-6; Sequence 6, Application US/09364230; Patent No. 6348339
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52.0%;
                                                                                                                                                                                                                                                                                                                                         Query Match 33.5%;
Best Local Similarity 48.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                               TYPE: PRT

CONGANISM: Escherichia coli

US-09-711-164-438
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; ORGANISM: Oryza sativa
US-09-364-230-6
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Matches 13; Conserv
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US-09-252-991A-29293
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Gaps

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GENERAL INCEMENTALON:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
FILE REPERBNGE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3137
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                                                                   DB 4; Length 466;
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                                                                      Score 62; DB '
Pred. No. 1.1;
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                                                                                                                     7; Mismatches
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                                                                                                                                                                                                                                                                                                                                  Sequence 3137, Application US/09134001C Patent No. 6380370
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3137
                                                                   Query Match 31.0%;
Best Local Similarity 42.3%;
Matches 11; Conservative
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Best Local Similarity 32.3%
Matches 10, Conservative
; ORGANISM: M.catarrhalis
US-09-540-236-2874
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US-09-134-001C-3137
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Patent No. 6673910
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 2709,2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
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Recent No. 6559294

GENERAL INFORMATION:
APPLICANT: Griffals, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                   WESOLI 2, 899-039A-10010
WS-09-489-039A-10010, Application US/09489039A
Sequence 10010, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF LILING DATE: 2709-22004001
CURRENT FILING DATE: 2709-2004001
CURRENT FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24 NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 31.5%; Score 63;
Best Local Similarity 35.5%; Pred. No. Matches 11; Conservative 7; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Klebsiella pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-489-039A-10010
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LENGTH: 466
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Appli
Sequence 3, Appli
Sequence 417, App
                                                                                                             September 16, 2004, 07:45:18 ; Search time 48 Seconds (without alignments) 254.231 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-067-482-3
US-10-067-482-3
US-10-067-482-4
US-10-167-5470-16
US-10-424-599-144794
US-10-437-963-116017
US-10-167-5470-14
US-10-437-963-116017
US-10-167-5470-14
US-10-767-701-52389
US-10-282-122A-45255
US-10-282-122A-45255
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                                                                                                                                                                                                                                                                                                                                 1342398 segs, 321133274 residues
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Maximum Match 100%
Listing first 100 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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uence 57891, uence 5781, uence 5781, uence 5781, uence 12590, uence 258895 uence 23837, uence 67387, uence 67387, uence 6155, uence 6155, uence 6155, uence 6155, uence 6155, uence 6155, uence 6155, uence 6155, uence 6158, uence 6168, uence 6168, uence 6168, uence 1831, uence 1831, uence 1831, uence 1868, uence 2087, uence 20870, uence 20870, uence 20870,	Thence 4516 Thence 20313 Thence 20313 Thence 2082 Thence 53203 Thence 53203 Thence 46495 Thence 46975 Thence 47502 Thence 53150, Thence 53150, Thence 53150, Thence 59189, Thence 59189, Thence 55983, Thence 62688,
US-10-282-122A-578 US-10-369-493-1197 US-10-369-493-1197 US-10-282-122A-456 US-0-815-42-2581 US-0-815-42-2581 US-0-815-42-12590 US-10-282-122A-439 US-10-282-122A-439 US-10-282-122A-591 US-10-282-122A-591 US-10-282-122A-591 US-10-282-122A-591 US-10-282-122A-591 US-10-282-122A-591 US-10-282-122A-591 US-10-282-122A-591 US-10-282-122A-591 US-10-282-122A-591 US-10-282-122A-591 US-10-282-122A-591 US-10-282-122A-691 US-10-369-493-1639 US-10-369-493-11508 US-10-282-122A-691 US-10-282-122A-691 US-10-282-122A-691 US-10-282-122A-691 US-10-282-122A-691 US-10-282-122A-692 US-10-369-493-11608 US-10-369-493-11608 US-10-369-493-11091 US-10-282-122A-6253 US-10-282-122A-6253 US-10-282-122A-6253 US-10-282-122A-6253 US-10-282-122A-6253 US-10-282-122A-6253 US-10-282-122A-6253 US-10-282-122A-633 US-10-282-122A-633 US-10-282-122A-633 US-10-282-122A-633 US-10-282-122A-633 US-10-282-122A-633 US-10-282-122A-733 US-10-282-122A-733 US-10-282-122A-733 US-10-282-122A-733 US-10-282-122A-733 US-10-369-493-1994 US-10-369-493-1994	US-10-425-114-4 US-110-424-599-2 US-110-424-599-2 US-110-282-1123A-10-282-1123A-10-435-114-4 US-110-425-114-5
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996 99 99 99 99 99 99 99 99 99 99 99 99	, , , , , , , , , , , , , , , , , , ,
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Query Match
Best Local Similarity 100.0
Matches 32; Conservative
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US-10-067-482-4
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CRGANISM: Homo sapiens
US-10-103-313-417
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Sequence 72073, A Sequence 72092, A Sequence 72099, A Sequence 8964, Ap Sequence 43, Appl Sequence 77672, A Sequence 61885, A Sequence 61885, A Sequence 7621, A Sequence 7621, A Sequence 7621, A
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; Sequence 3, Application US/10067482
; Sequence 3, Application US/10067482
; Publication No. US20030148407A1
; GENERAL INFORMATION:
    APPLICANT: OriGene Technologies, Inc.
    TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
    TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
    CURRENT APPLICATION WIMBER: US/10/067,482
    CURRENT FILING DATE: 2002-0-7
    NUMBER OF SEQ ID NOS: 4
    SOFTWARE: PatentIn version 3.1
    SEQ ID NO 3
    LENGTH: 547
                                                                                                                                                                                                                                                            Sequence 2, Application US/10067482;
Publication No. US20030148407A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
FILE REFERENCE: 1U 102 R1
CURRENT APPLICATION NUMBER: US/10/067,482
CURRENT PILIO DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 553
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                                                      US-09-875-573-43

US-10-369-493-20932

US-10-282-122A-7672

US-10-282-122A-61885

US-10-767-01-4125-

US-10-282-122A-61885

US-10-282-122A-61885

US-10-282-122A-70621

US-10-282-122A-70621
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    US-10-425-114-72073
US-10-425-114-72092
US-10-425-114-72099
US-10-369-493-8964
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100.0%; Pred. No. 1.5e-14;
trive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 32; Conservative
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Best Local Similarity 100.
Matches 38; Conservative
       485
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CRGANISM: homo sapiens
US-10-067-482-3
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ORGANISM: homo sapiens
       38.5
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US-10-067-482-2
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        RESULT 3
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US-10-167-547C-16
US-10-167-547C-16
US-10-167-547C-16
Sequence 16, Application US/10167547C
Sequence 16, Application Wolfolds3Al
GENERAL INFORMATION:
APPLICAMY: E.I. du Pont de Nemours and Company
APPLICAMY: Damude, Howard G.
TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
TITLE OF INVENTION: Butyrolactone and its Intermediates
TITLE OF INVENTION: Butyrolactone and its Intermediates
TITLE OF INVENTION: Butyrolactone and its Intermediates
TITLE OF INVENTION NUMBER: US/10/167,547C
CURRENT FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
SEQ ID NO 16
LENGTH: 289
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; Sequence 417, Application US/10103313;
publication No. US20030082758A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ07C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILIGO DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 417
LENGTH: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.0%; Score 166; DB 14; Length 550; 100.0%; Pred. No. 1.5e-14; tive 0; Mismatches 0; Indels (
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US-10-067-482-4
Sequence 4, Application US/10067482
Sequence 4, Application US/10067482
GENERAL INFORMATION:
APPLICANT: Oridene Technologies, Inc.
TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
FILE REFERENCE: 1U 102 R1
CURRENT APPLICATION NUMBER: US/10/067,482
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENTH: 276
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Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 31; Conservative 0; Mismatches 0;
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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Sequence 14, Application US/10167547C

Sequence 14, Application US/10167547C

Sequence 14, Application US/1016753A1

Sequence 14, Application US/1016753A1

Sequence 14, Application US/030170653A1

GENERAL INFORMATION:

APPLICANT: B. Jamude, Howard G.

APPLICANT: Banude, Howard G.

TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma

TITLE OF INVENTION: Butyrolactone and its Intermediates

FILE REFERENCE: CL1804 US NA

CURRENT APPLICATION NUMBER: 2003-03-17

PRIOR APPLICATION NUMBER: 60/297198

PRIOR APPLICATION NUMBER: 60/297198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT4530_19559C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GFLGLGIMGKAMAVNLLRSGFRVTVWNRTLSKCNELLE 41
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60.5%; Score 121; DB 16;
Best Local Similarity 64.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
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                                                                           Sequence 116017, Application US/10437963
Publication No. US20040123343A1
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                                                                                                                                                                                                                                           Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                              GENERAL INFORMATION
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A
APPLICANT: Buckharov, Andrey A
APPLICANT: Barbaruk, Brad
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SOFTWARE: Microsoft Office 07
SEQ ID NO 14
EBNOTH: 290
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Best Local Similarity 55.34
Matches 21, Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: tulip pistil
US-10-167-547C-14
                                                          US-10-437-963-116017
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US-10-437-963-174476
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APPLICANT: La Rosa Thomas J
APPLICANT: Avalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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                                             Score 125; DB 14; Length 289;
Pred. No. 4.1e-09;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.0%; Score 124; DB 12; Length 333; Best Local Similarity 64.9%; Pred. No. 6.7e-09; Matches 24; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.5%; Score 121; DB 16; Length 176; 64.7%; Pred. No. 8.5e-09; ive 4; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_101768C.1.pep
US-10-424-599-144794
                                                                                                                        GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                         4 GFLGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVE 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: 9298239.pep
US-10-767-701-60840
                                                                                                                                                                                                                                                                     ; Sequence 144794, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                             62.5%;
60.5%;
                         Query Match
Best Local Similarity 60.5%
Watches 23; Conservative
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine max
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LENGTH: 333
US-10-167-547C-16
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Best Local S
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 50561 LENGTH: 364
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: G0/191,078
PRIOR APPLICATION NUMBER: G0/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                              Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: LIB3136-019-H11_FLI.pep
US-10-425-114-50561
                                                                                                                                                                                                                                                                                                                                                 58.5%; Score 117; DB 12; 63.6%; Pred. No. 7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKC 33
                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 52083, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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PRIOR PILLING DATE: 2000-05-23
PRIOR PILLING DATE: 2000-05-23
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-09-06
PRIOR PILLING DATE: 2000-09-06
PRIOR PILLING DATE: 2000-09-09
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-11-27
PRIOR PULLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2001-12-22
PRIOR FILLING DATE: 2001-10-29
PRIOR FILLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Forsyth, R.
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Best Local Similarity 63.6
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trawick, John
Carr, Grant
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APPLICANT:
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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GENUERAL INFORMATION:
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TITLE OF INVENTION: Willier Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Willier and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
WUMBER OF SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_72412C.1.pep
US-10-437-963-174476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.5%; Score 117; DB 16; 63.6%; Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKC 33
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US-10-767-701-52389
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Publication No. US20040034888A1
GENERAL INFORMATION
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                           Kovalic, David K.
Exovalic, David K.
Exou, Yihua
Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
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                                                                                                                                                                              Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
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Best Local Similarity
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Best Local Similarity
Matches 21; Conserv
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US-10-425-114-50561
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US-10-767-701-52389
                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 174476
LENGTH: 293
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APPLICANT:
APPLICANT:
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APPLICANT:
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FILE REFERENCE: ELITRA, 034A

CURRENT APPLICATION: IMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-26

PRIOR PALING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-22

PRIOR PLING DATE: 2000-11-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-02-09

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 290;
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Pred. No. 2.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
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                             Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Trawick, John
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Best Local Similarity 59.4%;
Matches 19; Conservative
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
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APPLICANT:
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                                                                                    Gaps
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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      54.5%; Score 109; DB 12; Length 292; llarity 62.5%; Pred. No. 7.3e-07; Conservative 6; Mismatches 6; Indels
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53.0%; Score 106; DB 12; Length 288;
Best Local Similarity 55.6%; Pred. No. 1.9e-06;
Matches 20; Conservative 5; Mismatches 11; Indels
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                                                                                                                                                                  9 GFIGTGVMGKGMIKNLLKGGYTVHVYNRTKEK 40
                                                                                                                                 1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                 Sequence 45255, Application US/10282122A
Publication No. US20040029129A1
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PRIOR PELICATION NUMBER: 60/206, 848
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
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ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Wall, Daniel
Query Match
Best Local Similarity
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITRA.034A
CURRENT ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILIANG DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/283,625
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATORI, WASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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                                            Sequence 9081, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT CORGANISM: Streptomyces avermitilis US-10-156-761-9081
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Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
ARPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                 APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.03
Matches 16; Conservative
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APPLICANT:
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Sequence 11979, Application WS/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Garagory J.
APPLICANT: Glater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Glater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT S.
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    CURKENT APPLICATION NUMBER: US/10/282,122A
CURKENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-04
PRIOR PLING DATE: 2001-02-04
PRIOR PLING DATE: 2001-02-05
PRIOR PRIOR PLING DATE: 2001-02-06
PRIOR PLI
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CURRENT APPLICATION NUMBER: US/10/282,122A
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PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
ISO ID NO 11077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium US-10-282-122A-57891
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US-10-369-493-11979
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LENGTH: 475
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LENGTH: 295
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42.1%; Pred. No. 0.0011; tive 9; Mismatches 13; Indels

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                                                          16; Conservative
                             Best Local Similarity
Matches 16; Conserv
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APPLICANT:
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,335
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/203,335
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-11-27
PRIOR PLILNG DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLILNG DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLILNG DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLILNG DATE: 2001-0-20
PRIOR PLILNG DATE: 2001-0-20
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 56894
LENGTH: 296
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44.5%; Score 89; DB 12; Length 296;
Best Local Similarity 47.1%; Pred. No. 0.00047;
Matches 16; Conservative 7; Mismatches 11; Indels
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                     ) ORGANISM: Enterococcus faecalis
US-10-282-122A-56894
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ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
Wall, Daniel
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Length 464;

44.0%; Score 88; DB 12;

Query Match

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                                                                                                                                                                                                                                                                           APPLICANT: CAIL, GEALL U.

APPLICANT: Yamamoto, Robert T.

APPLICANT: XU, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR PRILOR DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION:
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :|| :|| : |: |::||::|| : 4 GVIGLAVMGKNLAWNIESRGYSVSVFNRSSEKTDLAVE 41
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44.0%; Score 88; DB 9;
Best Local Similarity 39.5%; Pred. No. 0.0011;
Matches 15; Conservative 12; Mismatches 11
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SOFTWARE: FastSEQ for Windows Version 4.0
Sequence 5781, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Staphylococcus aureus
                                                                                                                                  Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                   APPLICANT: Haselbeck, Robert
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APPLICANT: Cao Yongwei Applicant: Cao Yongwei Applicant: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 258895

LENGTH: 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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US-10-424-599-258895
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40.5%; Pred. No. 0.00033;
rative 10; Mismatches 12;
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR PEDILCATION NUMBER: 60/191,078
PRIOR PEDILCATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PEDILCATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-23
PRIOR PILING DATE: 2000-11-24
PRIOR PILING DATE: 2000-11-26
PRIOR PILING DATE: 2000-12-27
PRIOR PILING DATE: 2001-12-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kobert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Garr, Grant
APPLICANT: Rangento, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40.5%
Matches 15; Conservative
                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Glycine max
Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.0%; Score 88; DB 9; Length 468; 39.5%; Pred. No. 0.0011; ive 12; Mismatches 11; Indels
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44.0%; Score 88; DB 15,
Best Local Similarity 36.8%; Pred. No. 0.0011;
Matches 14; Conservative 13; Mismatches 1
                                                                                           PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-3
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
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      CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
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APPLICANT: La Rosa Thomas J APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 2943, Application US/10369493; Publication No. US20030233675A1
                                                 CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 47374
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Best Local Similarity 39.55
Matches 15, Conservative
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US-10-369-493-2943
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LENGTH: 469
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US-10-282-122A-43907

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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE NEFERENCE: ELITAA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/291,078

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-28

PRIOR PLING DATE: 2000-05-28

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/203,335

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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Pred. No. 0.0021;
19 GVVGLAVMGSNLARNFARNGNTVAVYNRSTDKTDKLI 55
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                                                                                                                                                          Sequence 60359, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAW, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDOS, SEIKO
APPLICANT: OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Listeria monocytogenes
                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Best Local Similarity 43.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                     Zyskind, Judith
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Trawick, John
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APPLICANT: McCormack, Ashling
APPLICANT: Stapleton, Cliona
APPLICANT: Stapleton, Cliona
APPLICANT: Burke, Kevin
TILLE OF INVENTION: Process for the preparation of L-amino acids using
TILLE OF INVENTION: Process for the preparation of L-amino acids using
FILE REFERENCE: 990229 BT-US-B
CURRENT APPLICATION NUMBER: US/10/686,736
PRIOR APPLICATION NUMBER: US/10-17
PRIOR APPLICATION NUMBER: US/10/078,167A
WITHER OF LINES DATE: 2002-02-22
                                                                                                  Gaps
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APPLICANT: Stapleton, Cliona
APPLICANT: Burke, Kevin
APPLICANT: Burke, Mevin
APPLICANT: Mockel, Bettina
TITLE OF INVENTION: Process for the preparation of L-amino acids using
TITLE OF INVENTION: a gene encoding 6-Phosphogluconate Dehydrogenase
FILE REFERENCE: 990229 BT-US-B
CURRENT APPLICATION NUMBER: US/10/078,167
NUMBER OF $\frac{AP}{AP}$C ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 459
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                              43.5%; Score 87; DB 12; Length 468; 39.5%; Pred. No. 0.0015; tive 12; Mismatches 11; Indels
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                                                                                                                                                                  6 GVIGLAVMGKNLAWNIESHGYSVSVFNRSSEKTDLMVE 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-686-736-3
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ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10686736
Publication No. US20040063181A1
GENERAL INFORMATION:
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                                                                                 15; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 43.28
Matches 16; Conservative
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                  RESULT 26
US-10-686-736-3
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LENGTH: 459
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RESULT 30
US-10-767-701-61555
US-10-767-701-61555
Sequence 61555, Application US/10767701
Fublication No. US20040172694A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE REPREBUCE: 38-21(53535)B
CURRENT FILLING DATE: 2004-01-29
UNDBER OF SEQ ID NOS: 63128
SEQ ID NO 61555
LENGTH: 154
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Best Local Similarity 40.5%; Pred. No. 0.00081;
Matches 15; Conservative 9; Mismatches 13; Indels
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Best Local Similarity 43.2%; Pred. No. 0.0022;
Matches 16; Conservative 8; Mismatches 13; Indels
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                                                                                                      APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE REPERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR PLICATION NUMBER: UP 99/377484
PRIOR PLICATION NUMBER: UP 99/377484
PRIOR PLILNG DATE: 1999-12-16
PRIOR PRILING DATE: 2000-04-07
PRIOR PLILNG DATE: 2000-04-07
PRIOR PLILNG DATE: 2000-08-03
PRIOR PLILNG PARE: 2000-08-03
PRIOR PARE: 2000-08-03
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US-10-767-701-61555
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US-09-738-626-5105
                                         TATEISHI, NAOKO
SENOH, AKIHIRO
APPLICANT:
APPLICANT:
APPLICANT:
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Search completed: September 16, 2004, 07:47:49 Job time : 51 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 100 summaries
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A, Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kuita, K.; Lapidus, A.; Lardinois, A, Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, R.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Y. M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Scanfon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanfon, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togmoni, A.; Tosato, V.; Uchiyama, A; Winters, P.; Yoshida, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Altheor: Rospikawa, H.F.; Zumarenin, B.; Yoshikawa, H.; Danchin, A. Danchin, A.; Asterence number: Asparance of the Gram-positive bacterium Bacillus subtilis. A; Residues; Preliminary; nucleic acid sequence not shown; translation not shown A; Residues E. 1288 KXUNA.

A; Residues; Preliminary; nucleic acid sequence not shown; translation not shown
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A; Status: preliminary
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3-hydroxyisobutyrate dehydrogenase homolog ykwC - Bacillus subtilis
3-hydroxyisobutyrate dehydrogenase homolog ykwC - Bacillus subtilis
5.5pecies: Bacillus subtilis
5.5pecies: Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: B69870
C;Accession: B69870
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
R;Kunst, F; Ogasawara, N; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Brulich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
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A, Recession: G97310
A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-292 «KUR»
A, Cross-references: GB:AE001437; PIDN:AAK81274.1; PID:g15026424; GSPDB:GN00168
C, Genetics: Clostridium acetobutylicum ATCC824
C, Genetics: Clostridium acetobutylicum ATCC824
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C;Species: Sulfolobus solfataricus
C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Accession: G90314
R;She, Q; Singh, R.K; Confalonieri, F; Zivanovic, Y; Allard, G.; Awayez, M.J.; Char Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus, Solfataricus complete genome.
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                                                                                                                                                                                                                                     YKWC B. subtilis ortholog
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 4.3e-07;
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Pred. No. 5.8e-07;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                             related to 3-hydroxyisobutyrate dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GFIGLGIMGFPMASNLLKAGYDLTVYNRTIEKAE 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 GFIGTGVMGKGMIKNLLKGGYTVHVYNRTKEK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match
Local Similarity 58.8%;
les 20; Conservative
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1 Similarity 62.5%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A99139
A;Accession: G90314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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A; Molecule type: DNA
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A;Gene: SSO1560
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dehydrogenase
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Matches
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor
A;Reference number: A82950; MUID:20437337; PMID:10984043
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A;Cross-references: GB:AE004646; GB:AE004091; NID:g9948213; PIDN:AAG05587.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
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                                                                                                                                     A;Gene: ykwC
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
F;5-266/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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A,Cross-references: GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13269.1; PID:g2633767
A,Experimental source: strain 168
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C; Accession: D33371

R; Stover. C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.

Nature 466, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable dehydrogenase PA2199 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Nov-2001
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                                                                                                                                                                                                                                                                                                                                           12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 GFIGLGVMGKSMASHILNDGHPVLVYTRTKEKAESILQ 43
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Best Local Similarity 52.9%; Pred. No. 1.3e-05;
Matches 18; Conservative 7; Mismatches 9
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.4%; Pred. No. 9.6e-06;
Matches 18; Conservative 8; Mismatches 12
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phosphogluconate dehydrogenase, decarboxylating (gnd) homolog - Lyme disease spirochete C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Bate: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 11-Jun-1999
C; Accession: H70169
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, B. Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. A; Authors: Smith, H.O.; Venter, J.C.
A; Authors: Smith, H.O.; Venter, J.C.
A; Reference number: A70100; MUID:98065943; PMID:9403685
                                                    A;Cross-references: EMBL:X58719; NID:g47524; PIDN:CAA41555.1; PID:g47525
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de
C;Keywords: oxidoreductase; pentose phosphate pathway
F;6-288/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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C.Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate deh
F;3-280/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate del
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R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; (C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Klaito, C.; Sekimizu, J. Lancet 357, 1225-1240, 2001

A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Ratus: preliminary A; A; Cocession: G89930

A; Status: preliminary A; MUD: 21311952; PMID: 11418146

A; Status: preliminary A; Mud. Coccus aureus. A; Mud. Coc
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A;Cross-references: GB:BA000018; PID:g13701310; PIDN:BAB42604.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
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C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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                                                                                                                                                                                                                                                                                     45.0%; Score 90; DB 1; Length 470; 43.2%; Pred. No. 0.00027; Live 10; Mismatches 11; Indels
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44.0%; Score 88; UB 2;
Best Local Similarity 42.1%; Pred. No. 0.0005;
Matches 16; Conservative 9; Mismatches 12
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                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 43.28
Matches 16; Conservative
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Best Local Similarity
15; Conserve
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Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilor A; Reference number: A95262; MUID:21396509; PMID:11481432

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Recession: G95277

A;Residues: 1-293 «KUR»

A;Residues: Barloy-Hubler, A; Abola, P.; Ampe, F.; Barloy-Hubler, D:; Hyman, R.W.; Joney, S.R.; Publer, A; Abola, P.; Ampe, F.; Barloy-Hubler, D: Hyman, R.W.; Joney, T. M.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Reflerence number: A96039; WUID:21368234; PMID:11474104
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                                                                                                                                                                                                                                                                       A,Map position: 4
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
F;40-301/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: G95277
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A;Molecule type: DNA
A;Residues: 1-334 <BEV.
A;Cross-references: EMBL:AL078470; GSPDB:GN00062; ATSP:F19B15.150
A;Experimental source: cultivar Columbia; BAC clone F19B15.
C;Genetics:
A;Gene: ATSP:F19B15.150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 334;
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Pred. No. 0.0001;
8; Mismatches 12; Indels
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Pred. No. 0.00016;
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Best Local Similarity 54.5%;
Matches 18; Conservative
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Best Local Similarity
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Matches
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Riclaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jonnes, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Scatus: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: lin1413
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate del
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C,Species: Listeria monocytogenes
C,Species: Listeria monocytogenes
C,Species: Listeria monocytogenes
C,Accession: AH1246
C,Accession: AH1246
C,Accession: AH246
A,Accession: AH246
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C,Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de
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A, Mesidues: 1-472 GLA>
A, Cross_references: GB:NC_003210; PIDN:CAC99454.1; PID:g16410792; GSPDB:GN00177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Cross-references: GB:AL592022; PIDN:CAC96644.1; PID:g16413886; GSPDB:GN00178
A, Experimental source: strain Clip11262
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Pred. No. 0.00095;
9; Mismatches 9; Indels
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Best Local Similarity 43.0%; Pred. No. 0.00095;
Matches 14; Conservative 9; Mismatches 9;
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1 Similarity 43.8%;
14; Conservative
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3. hydroxyisobutyrate dehydrogenase (B. subtilis YkwC protein) homolog lin1004 [imported]
C; Species: Listeria innocua
C; Accession: ACISSW
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshhi, H.
D; Jones, L.M.; Karst, U.
Science 294, 849-885. 2001
A; Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A; Reterence 204, 849-885. 2001
A; Authors: Rreft, U.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: ACISSW
A; Residues: 1-286 < GLA>
A; Residues: 1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 399, 323-329, 1999

A, Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A, Ascession: A72200; MUID:99287316; PMID:10360571
A, Accession: A72377
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-469 < ARN>
A, Residues: 1-469 < ARN>
A, Cross-references: GB:AE001722; GB:AE000512; NID:94980938; PIDN:AAD35523.1; PID:9498094
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C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de
F;5-285/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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                                                                                                                                                                                                                                                  6-phosphogluconate dehydrogenase, decarboxylating - Thermotoga maritima (strain MSB8) (Species: Thermotoga maritima (strain MSB8) (Species: Thermotoga maritima (c;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 (Spacesion: A72377 (Spa
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
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36.8%; Pred. No. 0.00051;
tive 13; Mismatches 11;
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 14; Conserv
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A; Molecule type: DNA

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A;Cross-references: GB:AE002301; GB:AE002160; NID:g7190372; FIDN:AAF39196.1; FID:g719037
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
                                                                         A;Gene: TC0333
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de
F;6-285/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
A,Residues: 1-299 <KOM>
A,Residues: 1-299 <KOM>
A,Experimental source: strain K12, W3110
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col.
A,; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - Escherichia coli (strain K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Map position: 68 min
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
C;Keywords: oxidoreductase
F;8-269/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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C; Species: Bscherichia coli
C; Species: Bscherichia coli
C; Accession: C91129
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Bytayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, R.; Hattori, M.; Shinagawa, H.
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome A; Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AB000394; GB:U00096; NID:g2367197; PIDN:AAC76159.1; PID:g1789513; A;Experimental source: strain K-12, substrain MG1655 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) homolog - Escherichia coli
N;Alternate names: hypothetical 31K protein (rnpB-sohA intergenic region)
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C;Accession: JQ0613; A65102
R;Komine, Y; Inokuchi, H.
submitted to JTPID, September 1990
A;Reference number: JQ0612
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                                                                                                                                                                                                            Length 479;
                                                                                                                                                                                        Query Match
42.5%; Score 85; DB 2; Length 479
Best Local Similarity 39.5%; Pred. No. 0.0013;
Matches 15; Conservative 11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A55102
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Matches 19; Conserv
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A;Residues: 1-299 <HAY>
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A; Residues: 1-479 <ARN>
A; Cross-references: GB: AE001620; GB: AE001363; NID: 94376631; PIDN: AAD18504.1; PID: 9437663
A; Cross-references: GB: AE001620; GB: AE001363; NID: 94376631; PIDN: AAD18504.1; PID: 9437663
B; Expad, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Akucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A; Feference number: A81500; MUID: 20150255; PMID: 10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-479 <REA>
A;Cross-references: GB:AE002201; GB:AE002161; NID:g7189316; PIDN:AAF38243.1; PID:g718932
A;Experimental source: strain AR39, HL cells
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 28-Jul-2000
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 28-Jul-2000
C;Accession: A81714
F;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Residues: 1-479-<STO>
A;Cross_references: GB:BA000008; NID:g8978732; PIDN:BAA98568.1; GSPDB:GN00142
A;Cross_references: strain J138
C;Genetics:
A;Gene: gnd
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate
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                                                                                                                                                                                                            Length 479;
                                                                                                                                                                                     Score 85; DB 2; Leman Pred. No. 0.0013;
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                                                                                                                                                                                                                                                                                                       1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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                                                                                                                                                                                                 42.5%;
42.1%;
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Best Local Similarity 42.15,
'-hea 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-479 <TET>
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C72088
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R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A; Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos A; Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Rosiduss: 1-295 cKUR>
A;Rosiduss: 1-205 cKUR>
A;Rosiduss: 1-205 cKUR>
A;Rosiduss: 1-205 cKUR>
A;Authors: Kahn, D:; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Authors: Kahn, D:; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Authors: Kahn, D:; Kahn, M.L.; Kalman, S.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Itle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Contents: annotation
                                                                                   probable dehydrogenase protein [imported] - Sinorhizobium meliloti (strain C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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46.9%; Pred. No. 0.0011;
iive 10; Mismatches 7
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Pred. No. 0.0011;
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Best Local Similarity 33.9%;
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: SMb20710
A;Genome: plasmid
C;Superfamilv: 2-b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable dehydrogenase yhaE [imported] - Escherichia coli (strain 0157:H7, substrain EDI probable dehydrogenase yhaE [imported] - Escherichia coli (5;Date: 16-Reb-2001 #sequence_revision 16-Reb-2001 #text_change 14-Sep-2001 (5;Date: 16-Reb-2001 #sequence_revision 16-Reb-2001 #text_change 14-Sep-2001 (5;Date: Na. N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew A;Tile: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.

A;Tile: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.

A;Reference number: A85480; MUD:21074935; PMID:11206551

A;Status: preliminary

A;Cacession: C85974

A;Cacession
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A;Cross-references: GB:AE000670; NID:g2982779; PIDN:AAC06408.1; PID:g2982783; GB:AE00065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ы
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A;Gene: hibD
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
F;3-265/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: yhaE
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
             A;Experimental source: strain 0157:H7, substrain RIMU 0509952
C;Genetics:
A;Gene: ECs44003
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whature 393-358, 1998
Mature 393.

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Recession: C70303

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.hydroxyisobutyrate dehydrogenase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 108 May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
C;Accession: C70303
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                --AEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Gaps
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                                                                                                                                                                                                                                 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 288;
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                                                                                                                                                                                                                                     Indels
strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 84.5; DB 2;
Pred. No. 0.00092;
                                                                                                                                                               Score 84.5; DB 2;
Pred. No. 0.00092;
9; Mismatches 9;
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Pred. No. 0.001;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches
                                                                                                                                                                                                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRT-
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ilarity 32.8%;
Conservative
                                                                                                                                                                             42.2%;
32.8%;
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                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 19; Conserv
                                                                                                                                                                             Query Match
Best Local Similarity
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Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
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Chaccesion: D6736

RyTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Authors, B16-820, 200

Alathors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.K.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, A; Mizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; Schwarz, C.M.; Venter, J.C.; Davis, R.W.
A; Mitle: Sequence and analysis of chromosome I of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Astatus, Preliminary
A; Miller, Davis, Lurian, M. M.
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C,Superfamily: 3-hydroxyisobutyrate dehydrogenase, 3-hydroxyisobutyrate dehydrogenase hc
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                                                                                                                                                                                                                                                                                                                    --AEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable dehydrogenase F23N20.16 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                       22;
                                                                                             Length 295;
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C; Genetics:

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A,Gene: gntZ
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate dek
C;Keywords: oxidoreductase; pentose phosphate pathway
F;5-284/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) [imported] - Brucella melitensis (strain c)species: Brucella melitensis (strain C)species: Brucella melitensis (c)bate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002 (c)Accession: AB3380 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; DalVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkvov, B.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesse Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensian Astrice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) [imported] - Salmonella enterica subsp. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: BE0897 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connetton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference number: AB0502; MUID:21534947; PMID:11677608
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C,Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AE008917; PIDN: AAL52205.1; PID: 917982987; GSPDB: GN00190
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                                                                                                                                                                                                                                                                     Pred. No. 0.0024;
5; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     6 GVIGLGVMGSNIALNMANKGENVAVYNYTRDLTDQLIQ
                                                                                                                                                                                                                                                                                                                                                                            1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 82.5; DB 2;
Pred. No. 0.0017;
                                                                                                                                                                                                                                       Score 83; DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 FLGLGVMGYPMAGHLKAKGGHDVTVYNRTAAK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FLGLGLMGSGIVSNL-LKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                    41.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.2%;
59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.2%;
32.8%;
                                                                                                                                                                                                                                                                     Best Local Similarity 44,7
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 59.4
les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superiamily. .... C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-291 <KUR>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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A; Cabarates: GB: AB005554; GB: D45242; GB: D31629; NID: G2280496; PIDN: BAA21576.1; PI R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berrer, C.; Bron, S.; Bronillet, S.; Bruschi, C.V.; Calduell, B.; Capuano, V.; Carter, N.M.; Cho A; Ehrlich, S.D.; Remerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, K.; Lu, H.; Masuda, S.; Harloo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Layono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Maneol, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle R; Rayer, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Saronlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sakowska, A.; Seron akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Winters, P.; Winpat, A.; Tamamane, R.; Yssummoto, K.; Yata, K.; Yata, K.; Yata, K.; Ata, K.; Atterence of the Gram-positive bacterium Bacillus subtilis.

A; Reference number: A69580; MUID:98044033; PMID:9384377
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T.; McDo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-488 <COL>
A;Experimental scores: GB:AE001213; GB:AE000520; NID:g3322606; PIDN:AAC65319.1; PID:g332260
A;Experimental source: strain Nichols
C;Genetics:
C;Genetics: TP0331
C;Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate delydrogenase homology <HTB.
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A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16045.1; PID:g2636555
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate;5-285/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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A; Fulle: Organization and transcription of the gluconate operon, gnt, of Back A; Reference number: A92561; MUID:87008613; PMID:3020045
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les 16; Conservative
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41.0%;
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Best Local Similarity 41.77
Matches 15, Conservative
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Best Local Similarity
Matches 15; Conserv
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A;Molecule type: DNA
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A,Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AB005176; PID:g12725281; PIDN:AAK06313.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Gentatios:
A;Genta: ywjF
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hq
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                                                                                                                                                       RESULT 27
(986901
hypothetical protein ywjF [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
c;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: G86901
R;Bolotin, A: Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
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                                       -AEKCDLFI 37
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Pred. No. 0.002;
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Indels
10;
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Best Local Similarity 43.8%; Freu. ...
Matches 14; Conservative 11; Mismatches
  Mismatches
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    Conservative
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A; Residues: 1-297 <STO>
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A;Molecule type: DNA
A;Residues: 1-293 <STC
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    19;
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RESULT 29

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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Lerge, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClells; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: C97687
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
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C,Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
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C,Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
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A;Reference number: A97359; MUID:21608551; PMID:11743194
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                                                                                                                                                                                                                                                                                                                                ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Residues: 1-300 «KUR»
A;Cross-references: GB:AE007869; PIDN:AAK88452.1; PID:g15157953; GSPDB:GN00169
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A;Experimental source: strain C58 (Dupont)
oxidoredutase [imported] - Agrobacterium tumefaciens (strain CS8, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AH2912
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Pred. No. 0.002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 16, 2004, 07:46:30 Job time : 16 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82;
Pred. No.
```

Q9chu6 lactococcus P96789 lactococcus P31937 homo sapien	O83973 treponema p P29266 rattus norv O99113 mus musculu	clost homo mus r	ovis ar	P77775 escherichia P45364 clostridium	P32185 oryctolagus	P52208 synechocyst O9xti0 caenorhabdi	P41572 drosophila	2415/3 drosophila Q92751 chlamydia p	Q8r9j3 thermoanaer 067049 amifex aeo	P41581 citrobacter P41582 citrobacter	P41574 escherichia P41575 klebsiella	P41577 klebsiella Q9zhd9 buchnera ap	027957 archaeoglob	US3814 MYCODACTETI P41583 citrobacter	P41578 shigella bo P41579 shigella dy P41580 chimella do	Q12680 saccharomyc	Q16836 homo sapien O61425 mis misculu	Poorts mus masses	Q9wvk/ rattus norv Q821m8 chlamydophi	Q8pqu9 xanthomonas	gesaks buciller ap Q811c5 bacillus an	P42205 pseudomonas P27412 rabbit hemo	P27413 rabbit hemo	P59961 mycobacteri P95113 mycobacteri	nterococ	acillus	acillus	299ul6 staphylococ	Q8nwm9 staphylococ	Q9kpq9 vibrio chol	Q89ww0 bradyrhizob	084719 chlamydia t	0883y4 pseudomonas				P56997 neisseria m P56985 neisseria m	neisseria				
1 6PGD LACLA 1 6PGD LACLC 1 D3HI HUMAN	<i>-</i>		1 6PGD SHEEP 1 GLXR ECOLI		D3HI		6PGD GPGD		1 GPDA_THETN 1 AROE_AQUAE			1 6PGD_KLETE 1 6PGD_BUCAP						1 HCDH_PIG		1 GPDA XANAC 1 6PGD RIICRP			1 Y12K_RHDV3		1 GPDA_ENTFA			GPD					GPDA_PSESM		TRK	PYRB	GAL	GALE		ALIGNMENTS		
472	335 335 335	332 482 482	482 292	297	3.5	299 299	481	334	330 269	445 445	44 445 545	445	269 294	44.5	4 4 4 4 4 5 5 6 6	2144	314 314	314	334	341 468	444	456	117	334	340 468	444	446	332	232	296	326 334	334	341	341 573	223	331	339 339	339				
36.5																																										
73 73 72 72	69 69 69	8 8 8 6	68	67 66.5	99	64	64 64	63	62 61	9	09 90	09	ი ი ი ი	. w r	, w w	58.5	58 58	71 07 88 88	000	20 C2	57.5	57	57	57	57	56.5	56.5 56.5	56	22	55	5 5 5	55	55	220	54	54	5.4 4.4	54				
4 E E E E E E E E E E E E E E E E E E E		0 H 44 44 4	44	45	747	49	50	52	54	5.5	58	59	61	63	99	67	69	70	7,7	74	75	77	78	80	81	83	80 08	986	88	000	97.0	92	93	95	96	97	2 60	100			E	
en Ltd.		7; Search time 10 Seconds (without alignments) 197.867 Million cell undates/sec			:DLF1Q 38				141681						by chance to have a he result being printed,	stribu			Description		P21577 synechococc	, 01	Q9V8ms drosophila Q931r3 staphylococ	Oppkx7 chlamydia m	222813 chiamydia p P23523 escherichia	083351 treponema p		P32142 escherichia O917c0 ealmonella	P31072 trypanosoma	P43774 haemophilus	P80859 bacillus su	084066 chlamydia t	F38/ZU Saccharomyc F70718 actinobacil	P28811 pseudomonas	Q9suc0 arabidopsis	V8cP4/ stapnylococ O60037 cunninghame	P37754 escherichia	P41576 klebsiella P14062 salmonella			P00350 escherichia P37756 shidella fl	
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen	n search, using sw model	September 16, 2004, 07:31:17; Sear (without) 197.867		10-08/-482-2_COPI_Z/I_308	GF LGEGEMGGGT VSNLLAMGHTVTVWNRTAEKCDLFTQ	BLOSUM62 Gardon 10 0 Gardott 0 c	· O Dependence · O control	41681 segs, 52070155 residues	s satisfying chosen parameters:	th: 0	M + C	continue March 1008 Maximum March 1008 Listing first 100 symmaries		t_42:*	the number of results predicted by than or equal to the score of the	nalysis of the	SUMMARIES	,	ch Length DB ID	5 288 1 YKWC	5 517 1	468 1 6PGD	468 1 6PGD_	1 479 1	294 1 GARR	488	467 1 6PGD	298	479 1	484	468 1 6PG2	084	484 1 6PGD	298 1 MMSB	468	485 1 6PGD	468 1 6PG9 7	468 1	481 1 6PGD_C	290 1 Y229	4 68 4 68	•
U	OM protein - protein	Run on: Sep		ct score: 20		Scoring table: BLOSUN	,	Searched: 141	Total number of hits	Minimum DB seq length: Maximum DB seq length:	. passing.				Pred. No. is the nu score greater than	4	e ³ t	0:	Score	99	89 44	88 44	87 43	85 42	9 84.5 42	0 84 42 1 83 41	2 81 40	4 80 40	5 80 40	7 80 40	79 39	96. 97. 0	1 77 38	2 75 37 3 75 37	4 75 37	5 75 37	6 74 37 7 74 37	, , 4 37 8 74 37	9 74 37	31 73 36.	3 73 36 3 73 36	

BY SIMILARITY

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Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
                   ACT SITE
SEQUENCE
                                                                                                                                                                                                                         RESULT 2
6PGD_SYNP7
                                                                                                        Matches
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      S FF S
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                                                                                                                                                                                                                                                                                                                                                  RAKULLINE-YBUJ44UJ3; FUDDWEGL=3J943/1;

RAKURST F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RAKURST F., Ogasawara N., Moszer I., Brans A., Braun M., Briggell S.C., Bron S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RACOISTER, Bourster I., Brans A., Braun M., Briggell S.C., Bron S.,

RABURST S., Eurschi C.V., Caldwell B., Capuano V., Carter N.M.,

RACOISTE, C., Ernington J., Fabret C., Ferrari E., Foulger D.,

RACOISTE, C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RACOISEPPI G., Guy B.J., Haga K., Haisech J., Harwood C.R., Henaut A.,

RAGISEPPI G., Guy B.J., Haga K., Haisech J., Harwood C.R., Henaut A.,

RAGISEPPI G., Guy B.J., Haga K., Hailo M.F., Itaya M., Jones L.,

RAGISEPPI G., Kohler P., Kollightly B.J., Grandi G.,

RAGISEPPI G., Kohler P., Kolligstein G., Krogh S., Kumano M.,

RACOIS B., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RAGIN N., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RAGIN N., Relock R., Lardinois S., Lauber J., Lazarevic V.,

RAGIN N., Relock R., Lardinois S., Lauber J., Lazarevic V.,

RAGIN N., Rivolta C., Rocha B., Roche B., Rey M., Reynolds S.,

RAGIN N., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scifone F.,

RAGIN N., Tacconi B., Purnelle B., Roche B., Rose M., Sator T.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Tanamacol H., Waitzareneger T.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Winters P., Wambutt R., Wadler B., Yanamaco K., Yata K.,

RA Winters P., Wambutt R., Wadler B., Yanamaco K., Yata K.,

RA Winters P., Wambutt R., Wadler B., Yanamaco G. the Gram-positive bacterium Bacillus R.,

RH The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                 STRAIN=168; Scanlan E.M.; Scanlan E. Devine K.M.; Scanlan E., Devine K.M.; Sequence of the Bacillus subtilis chromosome from ykuA to cse-15."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390:249-256(1997).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-2003 (Rel. 42, Last annotation update)
Hypothetical oxidoreductase ykwC (EC 1.1.-.-)
YKWC OR BSU13960.
                           288 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006183; 6FGD.
InterPro; IPR006115; 6PGD NAD.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRCNASE.
PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                             MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ222587; CAA10859.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z99111, CAB13269.1, -. PIR, B69870, B69870. Subtilist; BG13328; ykwC.
                               STANDARD;
                                                                                                                                              Bacillus subtilis.
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_TaxID=1423;
                           YKWC BACSU
034948;
                                                                                                                                                                                                                                                                                                                                  STRAIN=168
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CONFLICT 154 158 EPIVR -> SRSVP (IN REF. 1).

CONFLICT 407 407 R -> A (IN REF. 1).

CONFLICT 415 440 AAERGIPVPAFSASLDFFDSYRASPA ->

RONFLICT 419 452 DYFG -> TTC (IN REF. 1).

CONFLICT 449 452 BYFG -> TTC (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Culler D.C., Krogmann D.W.;
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESQUENCE FROM N.A., AND SUBSTRATE-BINDING SITE.
MEDLINE-90299831; PubMed=2113917;
Broedel S.E. Jr., Wolf R.E. Jr.,
"Genetic tagging, cloning, and DNA sequence of the Synechococcus sp.
strain PCC 7942 gene (gnd) encoding 6-phosphogluconate
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991 (Rel. 18, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                                              Length 288;
                                                                              49.5%; Score 99; DB 1; Length 288
47.4%; Pred. No. 9.1e-06;
tive 8; Mismatches 12; Indels
                     976DD9098DB47A30 CRC64;
                                                                                                                                                                                                    1 GELGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                          6 GPIGLGVMGKSMASHILNDGHPVLVYTRTKEKAESILQ 43
                                                                                                                                                                                                                                                                                                                                                                                                                      470 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR006114; 6PGD_C.
Interpro; IPR006113; 6PGD_decarbox.
Interpro; IPR006115; 6PGD_ND.
Interpro; IPR006184; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, MSS002, AAA27330.1, -.
EMBL, X58119, CAA41555.1; -.
EMBL, S14628, S14628.
HSSP, P00349, 2PGD.
InterPro, IPR008927, 6DGDH_C_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 172:4023-4031(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
172 172 B
288 AA; 30711 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGR00873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006183; 6PGD.
                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                VEGD SYNP7
P21577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family.
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Thu Sep 16 09:36:51 2004

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0
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=IFO 1060;
Watanabe M., Ishii N., Arisawa M., Aoki Y.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                       Length 470;
                                                45.0%; Score 90; DB 1; Length 470 ilarity 43.2%; Pred. No. 0.00023; Conservative 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.5%; Score 89; DB 1; Length 517; 39.5%; Pred. No. 0.00034; Live 9; Mismatches 14; Indels
   QW -> M (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91E3F520FFCABF7A CRC64;
                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                   1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                       517 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.5%; Pred. No. 0.000;
tive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P00349; 2PGD.
InterPro; IPR008927; 6DGDH C_like.
InterPro; IPR006183; 6PGD.
InterPro; IPR006114; 6PGD C.
InterPro; IPR006114; 6PGD Gecarbox.
InterPro; IPR006115; 6PGD MAD.
InterPro; IPR006115; 6PGD MAD.
InterPro; IPR006184; 6PGGOm BS.
Pfam; PF00348; NAD binding 2; 1.
PKINTS; PR0076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGREAMS; TIGRO0873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
Oxidoreductase; Pentose shunt; NADP.
                 470 AA; 50860 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB006102; BAA21690.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 AA; 56924 MW;
                                                                                                                                                                                                                                                                                                                                                 Candida albicans (Yeast).
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
     469
                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                               16;
                                                                                                                                                                                                                                  CANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family.
CONFLICT
                 SEQUENCE
                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                             Matches
                                                                                                                                                                                                                                  6PGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·.
                                                                                                                                                                                         STRAIN-N315;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchityama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanchisa M.,
Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lancet 359:1819-1827(2002).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-MW2;
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Naqai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Naqai Y., Iwama N., R.;
15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (BC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMs; TIGRO0873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 AA; 51802 MW; 61A5C2CAF3CCD011 CRC64;
                                                                                                                          Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.0%; Score 88; DB 1; 39.5%; Pred. No. 0.00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
                                                                                     Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain MW2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006114; 6PGD C.
InterPro; IPR006113; 6PGD decarbox.
InterPro; IPR006115; 6PGD NAD.
Pfam; PR00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; G89930; G89930.
HSSP; P00349; 2PGD.
WISS-2DPAGE; Q99TY2; STAAN.
InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR00817; 6PGDH_C_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006184; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP003134; BAB42604.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 39.58
                                                                    GND OR SA1342 OR MW1464.
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
SEQUENCE 468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acquired MRSA."
                                                                                                                                                                                                                                                                                                                                                                              aureus."
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1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38

ò

468 AA.

STANDARD;

6PGD_STAAN ID 6PGD_STAAN AC Q99T<u>Y</u>2;

2

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STAAM
                                                                                                                                                                                                                           family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP BIND
ACT SITE
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6PGD_STAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6PGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAM MEDLINNE=ZUJ96006; Fubbed=LU/Jall34;
RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Holt R.A., Evans R.A., Galle R.F.,
RA Adams M.D. Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Gorger R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazei R.G., Champe M., Pfeiffer B.D.,
RA Dallay R.M. Basu A.M. Baxendala J., Bayraktarogulu L., Bealey E.M.,
RA Bellaw R.M. Basu A.M. Baxendala J., Bayraktarogulu L., Bealey E.M.,
RA Berson K.Y. Banco P.V., Berman B.P., Bhandari D., Bolishakov S.,
RA Borkova D., Borchan M.R., Bouck J., Broketein P., Broiter P.,
RA Borkova D., Borchan M.R., Douck J., Broketein P., Broiter P.,
RA Dodson K.Y., Canley S., Dallike C., Davemport L.B., Davise P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Dodson K., J. Evangelista C.C., Ferraz C., Ferraz C., Ferraz C., Reischmann W.,
RA Dodson K.J., Harvey D.A., Heinman T.J., Hernardas G., Pelsischmann M.,
RA Hostin D., Houston K.A., Helman T.J., Wei M.-H., Iboeyam C.,
RA Lasko P., Lei Y., Leviteky A.A., Li J.H., Mill M., Kalush F., Karpen G.H., Kez J., Kaniman B.E.,
RA Lasko P., Lei Y., Molntcoh T.C., McLeodo J.W.,
RA Merkulov G., Milshina N.V., Mobary C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobary C., Morris J., Moshrefi A.,
RA Shieson K.A., Nisason M., Stupski M., Racheler F., Santh H.,
RA Syler E., Spradling A.C., Stapleton M., Stupski M., Sheller E., Spradling A.C., Stapleton M., Stupski M., Ranger C., Shen H.,
RA Shieson R.M., Woodeye T., Wenter K., Wang S., Zhu X., Smith H.O.,
RA Sheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.O.,
RA Gorder C., Thurer E., Moshref B., Sheng X.H., Zhong F.N., Woodes E., Sheng R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS, AND ALTERNATIVE SPLICING.
MEDINB=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield E.J. Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable 3-hydroxyisoputyrate dehydrogenase, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
         GVIGLAVMGKNLAWNIESRGYSVSVFNRSSEKTDLMVE 43
                                                                                                                          324 AA.
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                              1.1.1.31) (HIBADH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley;
                                                                                                                                          Q9V8M5; Q9V8M6;
16-OCT-2001 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lewis S.E.;
                                                                                                                               DROME
                                                                                                                                                                                                                                                                (EC 1.1
CG15093
                                                                                                                                 D3HI
                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAIVDASYDEMTADGVNKDTIFIDSSTISPDLVKSLQKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VROGLDANVF -> KCROGRPRVHGQEDHPLRRLWHGPGRQ
AVQOHDAGHLDDRCFGGHESGGAPGSRCQCLRRDHQLLHRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLĞLGDLQPCARSLPQCPSQQGLRRRFLLGSDHQGSGSGLR
SGQRFQLTHPAGISGAQGLPVAVR (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECMGKKITHCGVYGMGQAAKLCNNMMLAISMIGVSEAMNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKGARFIDAPVSGGVPGAEQATLTFMVGGTEAEYNAVKAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                           IsoId=Q9V8M5-2; Sequence=VSP_001281, VSP_001282;
SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GND OR SAV1511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROBABLE 3-HYDROXYISOBUTYRATE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
Hypothetical protein; Oxidotalouctase; NAD; Mitochondrion;
Transit peptide; Alternative splicing.
TRANSIT 1
25 MITOCHONDRION (RV STMITSDITEW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (in isoform Short). /FTId=VSP 001282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAD (ADP PART) (POTENTIAL).
BY SIMILARITY.
                             methyl-3-oxopropanoate + NADH.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 AA; 33883 MW; A39B534753EAE83E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus (strain Mu50 / ATCC 700699).
Bacteria: Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 87; DB 1; Ler
Pred. No. 0.0004;
                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTIG=VSP 001281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GFLGLGLMGSGIVSNLLKWGHTVTVWNRTABKCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches
                                                                                                                                                IsoId=Q9V8M5-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBGN0034390; CG15093.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006183; GFGD.
InterPro; IPR006115; GFGD.
Pfam; PF03446; NAD_binding_2; 1.
PRINTS; PR00076; GFGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=21311952; PubMed=11418146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003798; AAF57638.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003798; AAM68444.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
324
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196
227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196
195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
7
7
                                                                                                                                                                                   Name=Short;
                                                                                                                                      Name=Long;
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White Co., Hickey B.K., Peterson J., Uterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanto C., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba 'Hattori M., Ogasawara N., Hayashi H., Hiramatsu K., Shiba 'Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
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Bacteria; Chlamydiae; Chlamydia!es; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.5%; Score 87; DB 1; Length 468; 39.5%; Pred. No. 0.00057; ive 12; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          468 AA; 51783 MW; 07205599873133D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479 AA
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InterPro; IPR006183; 6PGD_C_like.
InterPro; IPR006184; 6PGD_C_B.
InterPro; IPR006114; 6PGD_C_InterPro; IPR0061113; 6PGD_decarbox.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006113; 6PGD_ND.
Pfam; PF03446; NAD_binding_2; 1.
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PRINTS; PR00076; 6PGDHDRGNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGRO0873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
                                                                                                                                                                                                                                                                                                                 Lancet 357:1225-1240(2001).
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nes 15; Conservative
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Matches
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CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Bacteria; Chlamydiae; Chlamydiales; Chlamydophila.
                                                                                         -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
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PROSITE; PS00461; 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.5%; Score 85; DB 1; Length 479
39.5%; Pred. No. 0.0011;
tive 11; Mismatches 12; Indels
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Last sequence update)
Last annotation update)
                                                              -!- PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006114; 6PGD_C.
InterPro; IPR0061115; 6PGD_ND.
InterPro; IPR0061115; 6FGD_NAD.
InterPro; IPR0061184; 6PGdom_BS.
Fram; PF00393; 6PGD], 1.
Fram; PF00393; 6PGD], 1.
Fram; PF003465; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
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30-MAY-2000 (Rel. 39,
10-OCT-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P00349; 2PGD.
TIGR; TC0333; -.
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SEQUENCE 479 AA;
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30-MAY-2000 (Re
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6PGD_CHLPN
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InterPro; IPR006115; 6PGD_NAD.
B3125 OR C3880.
            Escherichia coli, and Escherichia coli 06.
                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                           Geng M.M., Schubmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
Geng M.M., Schubmacher A., Marte R., Melchers K.,
Schneider S., Pohl T., Essig A., Marre R., Melchers K.,
The genome sequence of Chlamydia pneumoniae TW183 and comparison with
other Chlamydia strains based on whole genome sequence analysis.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-- CATALYTIC & CATIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
-- S-phosphate + CO(2) + MADPH.
-- TWALYTIC & TANDPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                      MEDLINE=20330349; PubMed=10871362;
Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome gequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                 -!- PATHWAY: Hexose monophosphate shunt.
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tartronate semialdehyde reductase) (TSAR).
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Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.5%; Score 85; DB 1; Length 479; 42.1%; Pred. No. 0.0011; ive 10; Mismatches 12; Indels
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    Nucleic Acids Res. 28:1397-1406(2000).
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InterPro; IPR006113; 6PGD decarbox.
InterPro; IPR006115; 6PGD NAD.
InterPro; IPR006115; 6PGD NAD.
Fam; PF00393; 6PGD; 1.
Pfam; PF00393; 6PGD; 1.
Pfam; PF00346; NAD binding 2; 1.
PRINTS; PR0076; 6PGDHDRGNASE.
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InterPro; IPR006183; 6PGD.
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EMBL; AE002201; AAF38243.1; --
EMBL; AE002546; BAA98568.1; --
EMBL; AE017158; AAP98300.1; --
PIR; C72088; C72088.
PIR; P66535; R86535.
HSSP; P00349; --
TIGR; CP0398; --
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Best Local Similarity
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                    [3]
SEQUENCE FROM N.A.
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01-NOV-1991
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GARR_ECOLI
ID GARR ECOLI
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                                                                                                                                                                                                                                                                                                                   Komine Y., Inokuchi H.; "Precise mapping of the rnpB gene encoding the RNA component of RNase P in Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=06.H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Roso D.J., Johou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
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"A common regulator for the operons encoding the enzymes involved in D-galactarate, D-glucarate, and D-glycerate utilization in Escherichia coli.";
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MEDLINE=98447507; PubMed=9772162;
Hubbard B.K., Koch M., Palmer D.R., Babbitt P.C., Gerlt J.A.;
Hubbard B.K., Koch M., Palmer D.R., Babbitt P.C., Gerlt J.A.;
"Evolution of enzymatic activities in the enclase superfamily: characterization of the (D)-glucarate/galactarate catabolic pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Mau B., Shao Y.;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 182:2672-2674(2000).
-!- CATALYTIC ACTIVITY: (R)-glycerate + NAD(P)(+) = 2-hydroxy-3-oxopropanoate + NAD(P)H.
-!- PATHRAY: D-galactarate metabolism; third step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
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InterPro, IPR006183, 6PGD.
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EMBL, U18997; AAA57928.1; ALT INIT.
EMBL, AE000394; AAC76159.1; ALT INIT.
EMBL, AE016767; AAN62321.1; ALT INIT.
ECOGENE; EG11176; GARR.
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                                                                                                                                                                                                                                                                                                                                                                                                                n Bscherichia coli K-12.";
Bacteriol. 173:1813-1816(1991).
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Biochemistry 37:14369-14375(1998)
                                                                                                                                                                                                                                                                                MEDLINE=91154140; PubMed=1705543;
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Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;

488 AA; 52767 MW; FB69CCCA98DEE6B5 CRC64;

Complete proteome. SEQUENCE 488 AA;

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SEE
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                                                                                                                                                                                                                                                                         Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren B., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                     21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
-!- PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRNU OR IECULI.
Treponema pallidum.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                               42.2%; Score 84.5; DB 1; Length 294; 32.8%; Pred. No. 0.00077; ive 9; Mismatches 9; Indels 21
InterPro; IPR006398; .a.t....
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
TIGRPAMs; TIGR01505; tartro sem red; 1.
TIGRPAMs; TIGR01505; tartro sem red; 1.
PROSITE: P800895; 3 HYDROXTISOBUT DH; 1.
Oxidoreductase; NAD; Complete proteome.
.... cTTE 170 30427 MW; 17DA392C2253278C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                      1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRT-----
                                                                                                                                                                                                                                                                                                                                                                                         488 AA
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InterPro; IPR006115; 6PGD NAD.
InterPro; IPR006184; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
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InterPro; IPR006183; 6PGD.
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Pfam, PF03446; NAD binding 2; 1.
PRINTS, PR00076; 6FGDHDKGNASE.
TIGREPAMS; TKGR00873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 281:375-388(1998).
                                                                                                                                                                             Query Match 42.2
Best Local Similarity 32.8
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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TIGR; TP0331; -.
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brischer L., Cumerton I.F., Cummings N.J., Daniel R.A.,
RA Brouillet S., Brisch K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Britz C., Fujita M., Fujita Y., Fumer S., Galizzi A., Galleron N.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Mibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazaravic V.,
RA Kobayashi Y., Koetter P., Mizuno M., Moestl D., Nakai S., Kumano M.,
RA Kurita K., Lapidus R., Liu H., Masuda S., Mauel C., Medigue C.,
RA Robayashi Y., Koetter P., Mizuno M., Moestl D., Nakai S., Ruk,
RA Robone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schretelle D., Porwollik S., Scrior P., Shin B.S.,
Sorvokin A., Tacconi E., Takagi T., Takahashi H., Takemati K.,
RA Sato T., Scanlan E., Schrete R., Scoffone F.,
RA Takeuchi M., Tamakoshi A., Tamakoshi A., Taramaka T., Tarahashi H., Weitzenegger T.,
RA Takauchi M., Wanbutt R., Wedler H., Weitzenegger T.,
RA Wanbutt R., Wedler E., Wedler H., Weitzenegger T.,
Wandhott R., Wandhott R., Wedler E., Yoshikawa H.F., Zusumoto K., Yasumoto K., Yasumoto K., Yata K.,
Robida K., Yoshikawa H.F., Zumareine R., Yoshikawa H.F., Zusumerein E., Poshikawa H.F., Zusumerein R., Poshikawa H.F., Dannian P., Poshikawa H.F., Zusumerein R., Poshikawa H.F., Zusumerein R., Poshikawa H.F., Zusumana R., Poshikawa H.F., Zusumana 
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96093926; PubMed=7584049;
Vosbitda K.-I., Seki S., Pujimura M., Miwa Y., Fujita Y.;
"Cloning and sequencing of a 36-kb region of the Bacillus subtilis
genome between the gnt and iol operons.";
                                                                                                                                                                                                                                                                                                                                     01-OCT-1989 (Rel. 12, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
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Fujita Y., Fujita T., Miwa Y., Nihashi J., Aratani Y.;
"Organization and transcription of the gluconate operon, gnt,
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                           6 GFIGLAVMGENLVLNIERNGFSVAVFNRTTTVVDRFL 42
    Score 84; DB 1;
Pred. No. 0.0015;
                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 261:13744-13753(1986) [2]
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                                                                                                                                                                                                                                                           6PGD_BACSU STANDARD, 1
P12013,
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequino-0CT-2003 (Rel. 42, Last anno
       42.0%;
Query Match
Best Local Similarity 43.2°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome between the gnt a DNA Res. 2:61-69(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / BGSC1A1;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
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Shigella flexneri
 STRAIN=BGSC5A2;
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Local Sim-
16;
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                                                                                                                MEDLINE=92065803; PubMed=1659648; Reizer J.; Reizer J.; Reizer A., Deutscher J., Saier M.H. Jr., Reizer J.; "Analysis of the gluconate (gnt) operon of Bacillus subtilis."; Mol. Microbiol. 5:1081-1089(1991).
--i- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
LOCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                                                                                                     -!- PATHWAY: H-excse monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                        Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
"36kb sequence between gntZ and trnY of B. subtilis genome.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.5%; Score 83; DB 1; Length 468; 44.7%; Pred. No. 0.0019; ive 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 AA; 51983 MW; 56D88BEB8E553856 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006114; 6PGD_C.
InterPro; PR006113; 6PGD_decarbox.
InterPro; IPR006115; 6PGD_NBD.
InterPro; IPR006184; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                Subtilist; BG10651; gntZ.
InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                             EMBL, J02584; AAA56927.1; -.
EMBL, AB005554; BAA21576.1; -.
EMBL, P99124; CAB16045.1; -.
EMBL, D78193; BAA11267.1; -.
PIR, D26190; D26190.
HSSP; P00349; 2PGD.
                                    SEQUENCE OF 460-468 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR00873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.7
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
            Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus licheniformis.
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SEQUENCE FROM N.A.
                                                                                                         PROBABLE FUNCTION.
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SEQUENCE 468 AA
                                                                                                                                                                                                                family.
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                                                 STRAIN=168;
   subtilis.
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BACLI
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6PGD_BA
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                                                                                                                             DAR Res. '1:157-162 (1994).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SECURENCE PROM N.A.

MEDILINE=93347669; PubMed=8346018;

Plunkett G. III. Burland V.D., Daniels D.L., Blattner F.R.;

Plunkett G. III. Burland a coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.";

Nucleic Acids Res. 21:3391-3398(1993).
                                  Yoshida K., Seki S., Fujita Y.; "Nucleotide sequence and features of the Bacillus licheniformis gnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=S.flexmeri, STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                  -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.5%; Score 81; DB 1; Length 467 42.1%; Pred. No. 0.0035; ative 6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-1993 (Rel. 27, Created)
01-0cT-1993 (Rel. 27, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
10-0cT-2003 (Rel. 42, Last annotation update)
10-0cT-2003 (Rel. 42, Last annotation update)
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InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006115; 6PGD_ND.
InterPro; IPR006184; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P00349; 2PGD.
InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
MEDLINE=96051988; PubMed=8535972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D31631; BAA06504.1; -. PIR; JC2306; JC2306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGRO0873; gnd; 1. PROSITE; PS00461; 6PGD; 1.
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Trypanosoma brucei
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NCBI_TaxID=5702;
                                                                                                                                                                family.
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"Utilization of dihydroorotate as sole pyrimidine source by Salmonella
                                                     "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441(2002).
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                            Infect. Immun. 71:2775-2786(2003).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                              Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Pournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Schwartz D.C., Blattner F.R., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., Complete genome sequence and comparative genomics of Shigella flexneri serctype 2a strain 2457T "; Infect. Immun. 71:2775-2786 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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EcoGene; EG11847; yihU.

InterPro; IPR002204; 3hydroxisobut_dh.

InterPro; IPR006115; 6PGD NAD.

PROMIT: PR00895; 3 HyDROXIISOBUT_DH; 1.

HyDchtetical protein; Oxidoreductase; NAD; Complete proteome.

ACT_SITE 171 HyDROXIISOBUT.
                                                                                                                     SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a; MEDLINE=22590274; PubMed=12704152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.0%; Score 80; DB 1; Length 298; 53.3%; Pred. No. 0.0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
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74FBC8C09FA7881C CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
18-EBB-2003 (Rel. 41, Last annotation update)
Hypothetical oxidoreductase yihU (EC 1.1.-.).
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EMBL, ARD000464; AAD13444.1; -.
EMBL, AEO15402; AAN45389.1; -.
EMBL, AEO16990; AAP18811.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 171 B
298 AA; 31158 MW;
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les 16; Conservative
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Q9L7S0;
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SEQUENCE
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SEQUENCE FROM N.A.

STRAIN=LT2 / SGSC1412 / ATCC 700720;

MEDLINE=11534948; PubMed=11677609;

MCDLINE=21534948; PubMed=11677609;

MCDLINE-21534948; PubMed=11677609;

MCDLILAND M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium"
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J. MOLL Biol. 282:667-681(1998).
---- CATALVIIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barrett M.P., le Page R.W.F.;
"A 6-phosphogluconate dehydrogenase gene from Trypanosoma brucei.";
Mol. Biochem. Parasitol. 57:89-100(1993).
                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:852-856(2001).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phillips C., Dohnalek J., Gover S., Barrett M.P., Adams M.J.; "A 2.8-A resolution structure of 6-phosphogluconate dehydrogenase
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28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.11.144)
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InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006115; 6FGD NAD.
InterPro; IPR006115; 6FGD NAD.
InterPro; IPR006015; NAD BS.
Pfam; PF03446; NAD binding_2; 1.
PR0SITE; P800895; 3 HYDROXYISOBUT_DH; 1.
Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
ACT SITE 171 HY SIMILARITY.
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MEDLINE=98411456; PubMed=9737929;
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01-JUL-1993 (Rel. 26, Last seq
28-FEB-2003 (Rel. 41, Last ann
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298 AA; 31280 MW;
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nes 15; Conservative
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6PGD_HAEIN
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                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.cib.ch).
                         SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                               PROSITE; PS00461; 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                                    PDB, 1PGJ; 11-NOV-98.
InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006133; 6FGD.
InterPro; IPR006114; 6FGD_C.
InterPro; IPR0061113; 6FGD_decarbox.
InterPro; IPR0061115; 6FGD_NDD.
InterPro; IPR0061184; 6FGD_NDD.
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Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                           EMBL; X65623; CAA46577.1; -. PIR; A48565; A48565.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Goodyne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.W. Utterback T.R., Hanna M.C., Spriggs T., Hedblom B., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Ghehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
-!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILMARITY: Belongs to the 6-phosphogluconate dehydrogenase family.
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FRE-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GND OR HI0553.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              52153 MW; 64FED260915ABC2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :||:||:||: | : | : | | : | | 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.0%; Score 80; DB 1; 39.5%; Pred. No. 0.0049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] SEQUENCE FROM N.A. STCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; Pabmed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U32737; AAC22210.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 39.5%
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNĎ OR HI0553.
Haemophilus influenzae.
479 AA;
  3322
3325
3362
3374
3377
3391
4401
4401
4401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BMBL; X99228; CAA67612.1; -.
BMBL; Z73041; CAA97285.1; -.
PIR; S64588.
HSSP; P00349; 2PGD.
GermOnline; 141568; -.
SGD; 500003488; GND2.
GO; GO:0004416; F:phosphogluconate dehydrogenase (decarboxyla. ..; IMP. GO; GO:000606; P:glucose metabolism; IGI.
InterPro; IPR008927; 6DGDH_C_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis of a 10.5 kb DNA fragment from the yeast chromosome VII reveals the presence of three new open reading frames and of a tRNAThr gene.";
Yeast 13:369-372(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
-!- PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
88-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating 2 (EC 1.1.1.44).
GND2 OR YGR256W OR G9170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: Hexose monophosphate shunt. SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                   Pfam; PF0039; 6FGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRONASE.
TIGREAMS; TIGR0073; gnd; 1.
PROSITE; PS00461; 6FGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97-79233; PubMed=9133741;
Mazzoni C., Ruzzi M., Rinaldi T., Solinas F., Montebove F.,
Frontali L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.0%; Score 80; DB 1; Length 484; 39.5%; Pred. No. 0.0049; Live 7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484 AA; 53140 MW; 8381EEB3C704C5DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
                                                                                                             PRT;
                                                                                   6DGDH_C_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                InterPro; IPR008927;
InterPro; IPR006183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
C64077; C64077
                            HSSP; P00349; 2PGD.
TIGR; HI0553; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 484 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6PG2_YEAST
ID __6PG2_YEAST
AC P53319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family.
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DDR READ DR RE
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A Kunst F., Ogsawara N., Absertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss E., Bruschi C.V., Cadwell B., Capuano V., Carter N.M., Brouillet S., Bruschi C.V., Cadwell B., Capuano V., Daniel R.A., Bronizot F., Deviner K.M., Dusterboft A., Ebrlich S.D., Emmerson P.T., A Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghinseppi G., Guy B.J., Hada K., Haicot J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamatea D., Kasahara Y., Klaerr-Blanchard M., Klein C., A. Joris B., Karamatea D., Kasahara Y., Klaerr-Blanchard M., Klein C., A. Joris B., Karamatea D., Kasahara Y., Klaerr-Blanchard M., Klein C., A. Joris B., Karamatea D., Kasahara Y., Klaerr-Blanchard M., Klein C., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Mosetl D., Nakai S., Noback M., Roote D., O'Reilly M., Portetelle D., Porwollik S., Prescott A.M., Rarco V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Rieger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y., Sandaie Y., Schuchi J., Sawlasha M., Serror P., Schin B.S., Soldo B., Sekiguchi J., Sakowska A., Serror P., Tognoni A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
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Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating II (EC 1.11.44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.0%; Score 80; DB 1; Length 492; 40.5%; Pred. No. 0.005; Artive 6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VOJI OR BSU23860.
Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                   3D75D53563987735 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 GLVGLAVMGQNLILNAADHGFTVVAYNRTQSKVDRFL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 AA
                                                                                                                                                                        Pfam; PP00333; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
TIGREAMS; TIGR00873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
Oxidoreductase; Pentose shunt; NADP.
InterPro; IPR006183; 6PGD.
InterPro; IPR006114; 6PGD C.
InterPro; IPR006113; 6PGD decarbox.
InterPro; IPR006115; 6PGD NAD.
InterPro; IPR0061184; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sporulation genes.";
Microbiology 142:3103-3111(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6PG2 BACSU STANDARD, P80859; P54546; 01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                   492 AA; 53922 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 40.5
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168 / JH642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6PG2_BACSU
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Davis R.W.;
                                                                                                                                                                                                                                                                                        family.
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P38720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6PG1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus ubtilis."
                                                                                                                                                                                                                                                           "First steps from a two-dimensional protein index towards a response-
regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-145(1997).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                              Medigue C., Rose M., Viari A., Danchin A.; "Detecting and analyzing DNA sequencing errors: toward a higher quality of the Bacillus subblils genome sequence."; Genome Res. 9:1116-1127(1999)
                                                                                                                                                                                                                                                                                                                              PATHWAY: Hexose monophosphate shunt.
SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                      family.
CAUTION: Ref.1 sequence differs from that shown due to a
frameshift in position 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00461; 6FGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                          STRAIN=168 / IS58;
MEDLINE=97443988; PubMed=9298659;
Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.5%; Score 79; DB 1; Length 468; 36.8%; Pred. No. 0.0065; Live 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L -> W (IN REF. 4).
Q -> E (IN REF. 1).
75268F6ED400F1BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 GVIGLAVMGKNLALNIESRGFSVSVYNRSSSKTEEFLQ 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Subrilist; BG11738; YqjI.
InterPro; IPR006183; 6PGD.
InterPro; IPR006114; 6PGD.C.
InterPro; IPR006113; 6PGD.decarbox.
InterPro; IPR006115; 6PGD.MAD.
InterPro; IPR006184; 6PGD.MAD.
Fam; PF00393; 6PGD; 1.
Pfam; PF00346; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D84432; BAA12615.1; ALT_FRAME.
EMBL; 299116; CAB14318.2; -.
HSSP; P00349; 2PGD.
                                                                                                                     MEDLINE=20036940; PubMed=10568751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51643 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIGRFAMS; TIGRO0873; gnd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                 SEQUENCE OF 1-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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ID 6PGD_CHLTR
AC 084066;
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480 AA

PRT;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                      STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 282:754-759(1998).

-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
-!- PATHWAY: Hex-CO(2) + NADPH.
-!- PATHWAY: Become monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating 1 (EC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
30-WAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
GND OR CT063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                            Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PTGRNTS; PR00076; 6PGDHDRGNASE.
TIGRPAMS; TIGR00873; 9nd; 1.
PROSITE; PS00461; 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.5%; Score 79; DB 1; Length 480
36.8%; Pred. No. 0.0066; Li Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 AA; 52667 MW; E2D9BFE893DCECB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006114; 6PGD_C.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006115; 6PGD_NAD.
InterPro; IPR006118; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AE001281; AAC67654.1; -.
PIR, A71561; A71561.
INSSP, P00349; 2PGD.
INTERPRO; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 36.8% hes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 480 AA;
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                                                                                                                                                                                                                     NCBI_TaxID=813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288C / AB972;
MEDLINES-94378003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATÄLYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
-!- PATHWAY: Hexose monophosphate shunt.
                                                                                                                                                                                                                           "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                        MEDLINE=95203288; PubMed=7895733;
Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.5%; Score 79; DB 1; Length 489; 40.5%; Pred. No. 0.0067; Live 6; Mismatches 16; Indels
                  Desouza M., Lobo Z., Maitra P.K.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55CAE5DACDC6A00B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGR00873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
Oxidoreductase; Pentose shunt; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                       Electrophoresis 15:1466-1486(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD_binding_2; 1.
                                                                                                                                                                                                                                                                                           SEQUENCE OF 41-47 AND 120-131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 AA; 53543 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z46631; CAA86600.1; -. EMBL; U00028; AAB68452.1; -. EMBL; U17155; AAAS3637.1; -.
                                                                                                                                                                                                                                                           Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 40.5 tes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S46671; S46671.
SEQUENCE FROM N.A.
                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         database.";
                                                                                                                                                                                                            Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 230:220-225(1997).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                   MEDLINE=97148607; PubMed=9020051;
Yoshida Y., Nakano Y., Yamashita Y., Koga T.;
"The gnd gene encoding a novel 6-phosphogluconate dehydrogenase and its adjacent region of Actinobacillus actinomycetemcomitans
                                                                            6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Pentose shunt; NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC_1992 (Rel. 24, Created)
01-DEC_1992 (Rel. 24, Last sequence update)
16-OCT_2001 (Rel. 40, Last annotation update)
3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) (HIBADH).
Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 AA; 53288 MW; F7BD0B2EA3BF624D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 GVIGLAVMGQNLILNMNDHGFKVVAYNRTTSKVDEFLE 45
                                                                                                                   Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 77; DB 1;
Pred. No. 0.012;
8; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JC5282; JC5282.
HSSP; P00349; 2PGD.
InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
InterPro; IPR006114; 6PGD_C.
InterPro; IPR0061114; 6PGD_C.
InterPro; IPR0061115; 6PGD_MAD.
InterPro; IPR0061115; 6PGD_NAD.
InterPro; IPR0061184; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF03446; NAD binding 2; 1. PRINTS; PR00076; 6PGDHDRGNASE.
                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seqn
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.5%;
36.8%;
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PROSITE; PS00461; 6PGD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D88189; BAA13558.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gluconate utilization;
                                                                                                                                     actinomycetemcomitans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00393; 6PGD;
Pfam; PF03446; NAD_bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sest Local Similarity
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        chromosomal DNA.
                                                                                                                                                                                      NCBI_TaxID=714;
6PGD_ACTAC
P70718;
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P28811;
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Gaps

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1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37

Matches

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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D3HI_ARATH STANDARD; PRT; 347 AA.

QSUGO; QBUCD5;

10-0CT-2001 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 4
                                                                                                                                      Steele M.I., Lorenz D., Hatter K., Park A., Sokatch J.R., Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO encoding methylmalonate-semialdehyde dehydrogenase and 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = methyl-3-oxopropanoate + NADH.
-!- PATHWAY: Distal valine metabolic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.5%; Score 75; DB 1; Length 298; 57.7%; Pred. No. 0.014; 7; Indels rive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
0C4D7B5A7C870730 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAD (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03446; NAD binding 2; 1.
PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
Oxidoreductase; NAD; Complete profeome
NP BIND
NAD (BY SIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FLGLGLMGSGIVSNLLKMGHTVTVWN 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 FLGLGNMGGPMAANLLKAGHRVNVFD 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; C42902; C42902.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006115; 6PGD_NAD.
                                                                                                                                                                                                                        Biol. Chem. 267:13585-13592(1992).
                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-92317087; PubMed=1339433;
                                                                                                                                                                                                       hydroxyisobutyrate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004778; AAG06957.1; -.
                  Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 AA; 30486 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        valine.
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hes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDUCTION: By
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Spermatophyra Magnollophyra; endicocyledons; core eddicots; rosids; core spermatophyra; Magnollophyra; endicocyledons; core eddicots; rosids; core and core
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PROSITE; PS00461; 6PGD; 1. Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;

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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;

"Genome-based analysis of virulence genes in a non-biofilm-forming

Staphylococcus epidermidis strain (ATC 12228).";

Mol. Microbiol. 49:1577-1593 (2003).

-!-CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose

5-phosphate + CO(2) + NADPH.

-!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·
0
                                                                                                                                                                                                                                                                                                      PROBABLE 3-HYDROXYISOBUTYRATE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.5%; Score 75; DB 1; Length 347; 39.5%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                            MITOCHONDRION (BY SIMILARITY)
                                                                                                                                            InterPro; IPR002204; 3hydroxisobut_dh.
PROSITE; PS00895; 3 HYDROXYISOBUT_DH; 1.
Hypothetical protein; Oxidoreductase; NAD; Mitochondrion;
Transit peptide. 34 MITOCHONDRION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Indels
                                                                                                                                                                                                                                                                                                                                                               NAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                               -> F (IN REF. 2).
6ED2E87CC3DE191C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 GFIGLGNMGFRMVNNLIRAGYKVTVHDINRDVMKMFTE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AE016748; AA004791.1; -.
InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
InterPro; IPR006184; 6PGD_C.
InterPro; IPR006114; 6PGD_C.
InterPro; IPR006114; 6PGD_C.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006113; 6PGD_MAD.
                                                         EMBL, AL080282; CAB45888.1; ALT SEQ.
EMBL; AL161554; CAB79093.1; ALT SEQ.
EMBL; AY086845; AAM63893.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            37364 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGR00873; gnd; 1.
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                                                                                                                                                                                                                                                                                                                                                               66
219
                                                                                                                                                                                                                                                                                                                                                                                         219 2
21
347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
Pubmed=12950922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GND OR SE1192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6PGD STAEP
Q8CP47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family.
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang R.F., Khan A.A., Cao W.W., Cerniglia C.E.;
"Identification and sequencing of a cDNA encoding 6-phosphogluconate
dehydrogenase from a fungus, Cunninghamella elegans and expression of
the gene in Escherichia coli.",
FEMS Microbiol. Lett. 169:397-402(1998).
-!-CATIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + ADDPH.
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
6-PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                             .
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                                                                          Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                             13; Indels
                                         468 AA; 52234 MW; A4738F224237494E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F7EGDDFF3D21EFB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Fungi, Zygomycota, Zygomycetes, Mucorales,
Cunninghamellaceae, Cunninghamella.
                                                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                6 GVVGLAVMGKNLAWNIESRGYSVSVYNRSRQKTDEMVK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 GLIGLAVMGONLILNMNDHGFVVCAYNRTTSKVDDFL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                            DB 1;
0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.5%; Score 75; DB 1; 37.8%; Pred. No. 0.023;
                                                                            37.5%; Score 75; DB:
34.2%; Pred. No. 0.02:
tive 12; Mismatches
                                                                                                                                                                                                                                                                   485 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMs; TIGRO0873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
Oxidoreductase; Pentose shunt; NADP.
OXIGNCE 485 AA; 53102 MW; F7E6f
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006114; 6FGD_C.
InterPro; IPR0066113; 6FGD_decarbox.
InterPro; IPR006115; 6FGD_NBD.
InterPro; IPR006184; 6FGGOm_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 36112;
MEDLINE=99085678; PubMed=9868787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03446; NAD binding 2; 1. PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y17297; CAA76734.1; -. HSSP; P00349; 2PGD.
                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 37.8 ses 14; Conservative
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                  Cunninghamella elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00393; 6PGD; 1
Pfam; PF03446; NAD_bin
                                                                                               Best Local Similarity
                             Complete proteome. SEQUENCE 468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.
                                                                                                                                                                                                                                                                   CUNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                RESULT 25
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6PG9_ECOLI

RESULT 26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nelson K., Selander R.K.;
"Intergeneric transfer and recombination of the 6-phosphogluconate dehydrogenase gene (gnd) in enteric bacteria.";
Proc. Natl. Acad. Sci. U.S.A. 91:10227-10231(1994).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
-!- PATHWAX: Hexcee monophosphate shunt.
-!- PATHWAX: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                     "Genomic organization of the Klebsiella pneumoniae cps region responsible for serotype K2 capsular polysaccharide synthesis in the virulent strain Chedid.";
J. Bacteriol. 177:1788-1798 (1995).
                                                         Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Klebsiella.
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
                                                                                                                                                                                                     MEDLINE=95204345; PubMed=7896702;
Arakawa Y., Wacharotayankun R., Nagatsuka T., Ito H., Kato N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Pfam; PF00393; GPGD; 1. | Pfam; PF00393; GPGD; 1. | Pfam; PF00393; GPGD; 1. | PRINTS; PR00446; NAD binding 2; 1. | PRINTS; PR00076; GFGDHDRGNĀSE. | TIGRAMB; TIGRO0873; gnd; 1. | GNGSITE; PS00461; GPGD; 1. | Gluconate utilization; Oxidoreductase; Pentose shunt; NADF. CONFLICT 316 316 G -> E (IN REF. 2). | CONFLICT 421 421 V -> F (IN REF. 2). | SEQUENCE 468 AA; 51328 MW; FFIEB557665FDC90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.0%; Score 74; DB 1; Length 468; 38.2%; Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD
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(Rel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR: DS6146; DS6146.
HSSP: P00349; 2PGD.
InterPro; IPR006183; 6PGD.
InterPro; IPR0661183; 6PGD.
InterPro; IPR0061113; 6PGD.
InterPro; IPR0061113; 6PGD.
InterPro; IPR0061115; 6PGD.
InterPro; IPR0061115; 6PGD.NAD.
InterPro; IPR0061184; 6PGGM.BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95024018; PubMed=7937867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D21242; BAA04786.1; -. EMBL; U14471; AAC43817.1; -.
                                                                                                                                                                                                                                                                                                                                                                                       12-456 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                          Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 13; Conserv
                                                                                                                                                          FROM N.A.
                                                                                                               NCBI_TaxID=573
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CW 7380
                                                                                                                                                                                  STRAIN=Chedid;
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ID _6PGD_SALTY
AC P14062;
DT 01-JAN-1990 (
DT 01-JAN-1990 (
                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation — the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol, 176:3126-3139(1994).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                        Jayarathe P., Bromner D., Maclachlan R.P., Dodgson C., Kido N., Whitfield C.; "Cloning and analysis of duplicated rfbM and rfbK genes involved in the formation of GDP-mannose in Escherichia coli 09:K30 and participation of K1b genes in the synthesis of the group I K30 capsular polysaccharide."; J. Bacteriol. 176:3126-3139(1994).
                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                  01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: Hexose monophosphate shunt.
-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.0%; Score 74; DB 1; Length 468; 38.2%; Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
                                                                                       468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 AA.
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InterPro; IPR006114; 6PGD.
InterPro; IPR006114; 6PGD decarbox.
InterPro; IPR006113; 6PGD decarbox.
InterPro; IPR006115; 6PGD MAD.
InterPro; IPR006118; 6PGD mBS.
Pfam; PF003446; MAD binding 2; 1.
Pfam; PF03446; MAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGMASE.
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=09:K30:H12 / E69;
MEDLINE=94252978; PubMed=7515042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L27646; AAA21136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR00873; gnd; 1. PROSITE; PS00461; 6PGD; 1.
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                                                                                       STANDARD;
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                                                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.
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ID 6PGD_KLEPN
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Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;

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STRAIN=LT2;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carsonce Did: Did: 1:213-222(1993).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
-!- PATHWAY: Hexose monophosphate shunt.
-!- SAMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILINE=94093871; PubMed=8269100;
Scott M.J., Kriticou D., Robinson A.S.;
Isolation of cDNAs encoding 6-phosphogluconate dehydrogenase and glucose-6-phosphate dehydrogenase from the mediterranean fruit fly Ceratitis capitata: correlating genetic and physical maps of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ceratitis capitata (Mediterranean fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Tephritoidea, Tephritidae, Ceratitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gluconate utilization; Oxidoreductase; Pentose shunt; NADP
                                                                                                                                                                      37.0%; Score 74; DB 1; Length 468; 38.2%; Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.0%; Score 74; DB 1; Length 481; 38.9%; Pred. No. 0.03;
                                                                                                   468 AA; 51395 MW; D8EBB53A2DAADBF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 AA; 52963 MW; FOABB506AD1B86D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 IGLAVMGQNLVLNMNDKGFVVCAYNRTVEKVNOFLK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                            1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                     10; Mismatches
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InterPro; IPR008927; GDGH_C_like.
InterPro; IPR006.18; 6PGD.
InterPro; IPR006.113; 6PGD_C.
InterPro; IPR006.113; 6PGD_decarbox.
InterPro; IPR006.115; 6PGD MAD.
InterPro; IPR006.115; 6PGD MAD.
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PEam; PP03446; NAD binding 2; 1.
PRINTS; PR00076; GPGDHDRGNASE.
TIGRFAMS; TICR00873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
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Matches 14; Conservative
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Best Local Similarity
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SEQUENCE 468 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=LTZ (SGSC1412 / ATCC 700720;
MEDLINE=LTZ (SGSC1412 / ATCC 700720;
MEDLINE=LTZ STRAIN=LTZ (SGSC1412 / BENDLINE=LTZ (SGSC1412 / BENDLINE=LTZ (SGSC1412 / BENDLINE=LTZ (SGSC1412 / BENDLINE)
COURTING L., POTWOILIK S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE=91260454; PubMed=1710759;
MEDINE=91260454; PubMed=1710759;
Jiang X.M., Neal B., Santiago F., Lee S.J., Romana L.K., Reeves P.R.;
"Structure and sequence of the rfb (O antigen) gene cluster of
Salmonella serovar typhimurium (strain LT2).";
Mol. Microbiol. 5:695-713(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose 5-phosphate + CO(2) + NADPH.
-!- PATHWAY: Hexose monophosphate shunt.
-:- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                          Reeves P., Stevenson G.; "Cloning and nucleotide sequence of the Salmonella typhimurium LT2 and gend gene and its homology with the corresponding sequence of Escherichia coli K12.", Mol. Gen. Genet. 217:182-184(1989).
                                                                                                                                         Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBL_TaxID=602;
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (BC 1.1.1.44)
GND OR STM2081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dykhuizen D.E., Green L.;
Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases.
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HSSP; P00349; 2PGD.
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                                                                                                                    Salmonella typhimurium.
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IPR008927; 6DGDH_C_like.

InterPro; InterPro; InterPro;

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RA WOOD V., GWILLIAB JABON B.

RA WOOD V., GWILLIAB W., Rajandream M.A. Lyne M., Lyne R., Stewart A., RA GOOL V., GWILLIAB JABON D., Barker S., Baker S., Basham D., Bowman S., Brocks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA GOLLIAB M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Jones L., Jones M., Leather S., McDonald S., McLean J., RA Jones K., Jones M., Leather S., McDonald S., McLean J., RA Jones K., O'Neil S., Mundall K., Murphy L., Niblett D., Odell C., RA Cliver K., O'Neil S., Mandall K., Ruthy L., Niblett D., Odell C., Ra Cliver K., O'Neil S., Mandall K., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Carynomprez B., Woodward J., Volckeart G., Aert R., Robben J., Grymonprez B., Weltjens I., Volckeart G., Aert R., Robben J., Grymonprez B., Weltjens I., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Egrr P., Zimmernann W., Wedler H., Wahult R., Purnelle B., Galter B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Loras M., Loas M., Rochet M., Galilardin C., Tallda V.A., Garzon A., Thode G., Loas M., Rochet M., Galilardin C., Tallda V.A., Garzon A., Thode G., Loas M., Rochet M., Galilardin C., Tallda V.A., Garzon A., Thode G., And R. A., Bayakovski G.V., Ussery D., Barrell B.G., Nurse P., Revuelta J.L., Moreno S., Armstrong J., Potsburg S.L., Revuelta J.L., Moreno S., Armstrong J., Potsburg S.L., Revuelte J., Machel P., Nachel 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.; "Identification of open reading frames in Schizosaccharomyces pombe

        EPGD SCHPO
        STANDARD;
        PRT;
        492 AA.

        P78812;
        Q9UQMS;
        L15-JUL-1998 (Rel. 36, Created)
        L6-OCT-2001 (Rel. 40, Last sequence update)

        16-OCT-2001 (Rel. 41, Last annotation update)
        28-FEB-2003 (Rel. 41, Last annotation update)
        6-phosphogluconate dehydrogenase, decarboxylating (EC 1.11.44).

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-!- SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                       SPBC660.16.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales;
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DNA Res. 4:363-369(1997).
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                                                   6PGD_SCHPO
RESULT 30
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EMBL; D89161; BAA13823.1; ALT_INIT.

GeneDB SPombe; SPBC660.16; -. EMBL; AL034563; CAA22536.1; PIR; T40628; T40628. HASSP; P00349; 2PGD.

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492 AA; 53679 MW; FS5F342957A9D3E1 CRC64;
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                                                                                                                                                                                                                         37.0%; Score 74; DB 1; 37.8%; Pred. No. 0.031;
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ive 7; Mismatches
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                       InterPro; IPR006114; 6PGD_C.
InterPro; IPR006115; 6PGD_NAD.
InterPro; IPR006115; 6PGD_NAD.
InterPro; IPR006118; 6PGGO_NAD.
InterPro; IPR006184; 6PGGOM_BS.
Pfam; PP00346; NAD binding 2; 1.
Pfam; PF03446; NAD binding 2; 1.
                                                                                                                             TIGREAMS, TIGRO0873, gnd, 1.
PROSITE; PS00461; 6PGD; 1.
Oxidoreductase; Pentose shunt; NADP.
CONFLICT 219 220 IA -> S7
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0811r8 pseudomonas
089ha0 bradythizob
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081835 bacillus an
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070xfp7 bordetella
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070xfp7 bordetella
070xfp8 bordetella
080xfl xanthomonas
080xfl xanthomonas
070xjp8 bordetella
080xjp8 thermoanaer
070xjp8 bordetella
080xjp9 borrelia bu
095td04 streptomyce
051509 borrelia bu
095ty2 staphylococ
090xyfp deseudomonas
080fy2 dresphila
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Q9c990 arabidopsis
Q8ubw3 agrobacteri
Q8Aq44 streptomyce
Q949m8 arabidopsis
Q88aS listeria mo
Q88rx1 encephalito
Q8173 agrobacteri
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Q876c3 saccharomyc
Q876c3 saccharomyc
Q97ze5 sulfolobus
Q8x8d4 escherichia
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Q8170 oryza sativ
Q8vlm3 anabaena sp
Q9ngrO leishmania
Q9ngr1 leishmania
Q9ngr1 leishmania
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0931E3
089UU4
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Q89M84
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Q8XAE4
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QBUF73
QB75M5
QB75M5
QB76H8
Q97ZE5
Q97ZE5
Q8Z2T6
QBLQ70
QRVRX5
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Q922p9 mus musculu Q9cyq1 mus musculu Q9bxk2 homo sapien Q8t079 drosophila Q94a74 arabidopsis Q94a74 arabidopsis Q91wV1 arabidopsis Q81wV1 arabidopsis Q81wp0 arabidopsis Q81my0 cryza sativ Q97dx8 clostridium Q97xz7 sulfolobus Q92n92 thizobium m Q8tt25 methanosarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9btil homo sapien
                                                   2004, 07:30:52; Search time 39 Seconds (without alignments) 307.428 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                    1017041
   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                     1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
                                                                                                                                                               of hits satisfying chosen parameters:
                                                                                                                                               1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                     US-10-067-482-2_COPY_271_308
                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                     sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0922P9
09CYQ1
09BXK2
08T079
094A74
094B07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBRWF1
Q9LNP0
Q8LQJ7
Q84VC8
Q97DX8
Q97XZ7
Q97XZ7
                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                         sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9BTI1
                                                                                                                                                                                                                                                                                    sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                   - protein search, using
                                                                                                                                                                                                                                                                                                                                                                           sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                              sp_organelle:*
                                                                                                                                                                                                                                                   sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                               sp_plant:*
sp_rodent:*
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                                                                                                                                                                                                                                                                                                                                                 sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                           SPTREMBL_25:*
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                                                     September 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match
                                                                                                                                                                                                                                                                                                             88:
1010:
1121:
113:
114:
116:
                                                                                    Title:
Perfect score:
                                                                                                                      Scoring table:
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666
1066
1025
1023
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1031
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1031
                                                                                                                                                               Total number
                                  OM protein
                                                                                                      Sequence:
                                                                                                                                              Searched:
                                                                                                                                                                                                                                          Database
                                                   Run on:
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MALLIADE-LIADODORO, TUDDING-LIADODORO, ILOD M., IShii Y.,
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Salto T., Lewis S., Marsuo Y., Nikanio I., Rochiwa H.,
RA Schriml L. Lewis S., Marsuo Y., Nikanio I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaetts P.,
Rodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1921272; Npac.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                              MGD; MGI:1921272; Npac.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004616; F:phosphognomate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:pencose-phosphate shunt; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.0%; Score 166; DB 11; Length 546; 100.0%; Pred. No. 4.3e-13;
                        Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006893; AAH06893.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           59715 MW; F5D2090DE1F64723 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 GFLGLGLMGSGIVSNLLKWGHTVTVWNRTAEK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                       InterPro; IPR006115; 6PGD NAD.
InterPro; IPR000637; AT hook.
InterPro; IPR000313; PWWP_domain.
                                                                                                                                                                                                                                                                                                                                     Pfam; PF02178; AT hook; 1.
Pfam; PF03446; NAD_binding_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
EMBL; AK014456; BAB29363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00384; AT hook; 1.
PROSITE; PS50812; PWWP; 1.
SEQUENCE 546 AA; 59715 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPAC OR 3930401K13RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3930401K13Rik protein
                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00855; PWWP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9CYQ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
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                                                                                $92pa2 rhizobium m Q8fbg0 escherichia Q8fbg0 escherichia Q8yax brucella me Q8fxg6 brucella su Q9ckq2 pasteurella Q7vmx4 haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC003634; AAB03633.1; —...

GO; GO:0005634; C:nucleus; IEA.

GO; GO:000567; F:DNA binding; IEA.

GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. ..; IEA.

GO; GO:0006098; P:pentose-phosphate shunt; IEA.

GO; GO:0006098; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR006115; GFGD NAD.

InterPro; IPR000113; PWWP domain.

Pfam; PF00179; AT hook; 1.

Pfam; PF00185; PWMP; 1.
                                                           spinacia ol
                                  mycobacteri
                                                                                                                                                                                                                                                                    2876h9 saccharomyc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                  P95165
Q94ku2
             28vjv7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57215 MW; ED3E2853938A211F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 200; DB 4;
100.0%; Pred. No. 1.6e-17;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similar to RIKEN cDNA 3930401K13 gene (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                523 AA
                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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                                                                                                                                           Q8YAX7
Q8FXG6
Q92P61
                                                                                                                                                                                                                      Q9CKQ2
Q7VMX4
                                                                Q94KU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                   Q8FBG0
                                                                                           292PA2
                7VJV8C
                                          995165
                                                                                                                                                                                                                                                                            0876H9
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01-DEC-2001 (TrEMBLrel. 19,
01-OCCT-2003 (TrEMBLrel. 25,
RIKEN CDNA 3930401KL3 gene.
NPAC OR 3930401KL3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART, SM00384; AT hook; 1.
PROSITE; PS50812; PWWP; 1.
                  16
116
116
116
116
116
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Best Local Similarity 100.0°
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                40.0
440.0
440.0
339.8
339.5
339.5
399.5
399.5
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79.5
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RESULT 2 Q922P9

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ID DT DT DT OC OC OC OC OC OC

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Gaps

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O9BTI1

RESULT 1

Q9BTI

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Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004616; P:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                    Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 547;
                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                    59744 MW; B3AC1562477ABC1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59827 MW; C7D785CCBF83204A CRC64;
                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 166; DB 4; L
Pred. No. 4.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                                                   Score 166; DB 11;
Pred. No. 4.3e-13;
                                                                                                                                                              270 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.0%; Scor.
100.0%; Pred. No. 3.
                                                                                                                                           1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                547 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602 AA.
                                                                                                        100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LD22344p (CG4747-PA).
BEST:LD22483 OR BEST:LD29743 OR CG4747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last anno
                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                Cytokine-like nuclear factor n-pac.
Homo sapiens (Human).
InterPro; IPR006115; 6PGD NAD.
InterPro; IPR000637; AT hook.
InterPro; IPR000313; PWWP_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006115; 6PGD NAD.
InterPro; IPR000637; AT hook.
InterPro; IPR000313; PWWP_domain.
                             Pfam; PF02178; AT hook; 1.
Pfam; PF03446; NAD binding 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02178; AT hook; 1.
Pfam; PF03446; NAD binding_2; 1.
                                                                                                                                                                                                                                                                                                                                                                             GO; GO: 0005634; C: nucleus; IEA.
                                                 Pfam; PF00855; PWWP; 1.
SMART; SM00384; AT hook; 1.
PROSITE; PS50812; PWWP; 1.
SEQUENCE 546 AA; 59744 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00855; PWWP; 1.
SMART; SM00384; AT hook; 1.
PROSITE; PS50812; PWWP; 1.
                                                                                                    83.0%;
                                                                                                   Query Match
Best Local Similarity 100.
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8T079; Q9VL51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                               O9BXK2
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REALDELINE-20196006; PubMed=10731132;

RADELINE-20196006; RADELINE-1, RADELINE
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                                                                                           Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY069497; AAL39642.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
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Nakamura Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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EMBL; AE003627; AAF52846.3; -.
PyBase; FB900043466; BEST:LD22483.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla...; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
InterPro; IRRO00115; FGPGD NAD.
InterPro; IRRO00115; FWWP_domain.
Pfam; PF03446; NAD_binding_2; 1.
Pfam; PF03486; WWP; 1.
PROSITE; SA00123; PWWP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Kim C.J., Chen H., Cheuk R., Koesema B., Meyers M.C., Banh J.,

Kim C.J., Chen H., Cheuk R., Koesema B., Meyers M.C., Hayashizaki Y.,

Ishida J., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Kawai J., Lam B., X., Jones T., Kamiya A., Karlii-Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,

Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,

Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   AT3g25530/WML2_15.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO, GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:00064616; F:phosphogluconate dehydrogenase (decarboxyla. . .;
GO; GO:0006098; P:pencose-phosphate shunt; IEA.
GO; GO:0006573; P:valine metabolism; IEA.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR002183; 6PGD_NAD.
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                                                                                                                                                                       Length 602;
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                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Arabidopsis cDNA clones.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY049298; AAK83640.1;
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PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
SEQUENCE 248 AA; 26336 MW; C96912B3E2A7E677 CRC64;
                                                                                                                                           65252 MW; E004EEC610C23625 CRC64;
                                                                                                                                                                                                                                                319 GFLGLGMMGSTIVKDLIYTGHKVVVWNRTIDKCQPFAE 356
                                                                                                                                                                                                                                                                                                                                                         (Tremblrel. 19, Created)
(Tremblrel. 19, Last sequence update)
(Tremblrel. 24, Last annotation update)
                                                                                                                                                                                                                               1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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                                                                                                                                                                                                   10;
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Pred. No. 3.9e-08;
                                                                                                                                                                       Score 126; DB 5;
Pred. No. 7.4e-08;
                                                                                                                                                                                                                                                                                                                                248 AA
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                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                PRT;
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60.5%;
                                                                                                                                                                      63.0%;
60.5%;
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Best Local Similarity 60.5
Matches 23; Conservative
                                                                                                                                                                                                   23; Conservative
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                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                            602 AA;
                                                                                                                                                                                      Local Similarity
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01-DEC-2001
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                                                                                                                                            SEQUENCE
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                               Q94A74;
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Q94B07; 01-DEC-2001 (TrEMBLrel. 19, Created)

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EMBL; AY044183; AAK94781.1; EMBL; Proxidorate dehydrogenase activity; IEA. GO; GO:00044015; Proxidorate dehydrogenase (decarboxyla...; IEA. GO; GO:000679; Proathose-phosphate shunt; IEA. GO; GO:000679; Proathose-phosphate shunt; IEA. InterPro; IPR006183; GPGD. InterPro; IPR006183; GPGD. InterPro; IPR006183; GPGD. AD. Pfam; PR0178; PR00076; GPGDHRQAAG, PR0178; PR00076; GPGDHRQAAG, PR0178; PR00076; GPGDHRQAAG, PR0178; PR00096; 3_HYDROXXISOBUT_DH; 1.
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BMBL, AB025639; BAB01322.1; -.

GO, GO:0006442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.

GO, GO:00064616; F:3-hosphogluconate dehydrogenase (decarboxyla. . .; IEA.

GO; GO:0006098; P:pentose-phosphate shunt; IEA.

GO; GO:0006573; P:valine metabolism; IEA.

InterPro; IPR002204; 3hydroxisobut_dh.

InterPro; IPR006183; 6FGD.
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                                                                                                                                                                                              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Gamma hydroxybutyrate debydrogenase (EC 1.1.1.61).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                 [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Breitkreuz K.E., Van Cauwenberghe O.R., Allen W.L., Jakobs C.,
Talibi D., McLean M.D., Andre B., Shelp B.J.;
"Plant gamma-hydroxybutyrate dehydrogenase, a novel fermentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis of Arabidopsis thaliana chromosome 3. I. Se features of the regions of 4,504,864 bp covered by sixty Pl and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.5%; Score 125; DB 10; 60.5%; Pred. No. 4.5e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzyme.";
Submitted (JUL-2001)
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es 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
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Gaps

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Mismatches

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1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD
                                            55 GFLGMGIMGSPMAQNLIKAGCDVTVWNRTKSKCD
22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                        01-OCT-2000
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Shabidopsis ORF clones."
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Cheuk R., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawi J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Kawi T., Sartou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Scher J., Theologis A., Davis R.W.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY093135; AAM13134.1; -.
EMBL; AX085690; AAM62909.1; -.
EMBL; BT008734; AAP42747.1; -.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla., GO; GO:0006098; P:pentose_phosphate shunt; IEA.
                                                                                                                0
                                                                                  Score 125; DB 10; Length 289;
Pred. No. 4.5e-08;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haās B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Stefdmann K.; Frail-Length CDNA from Arabidopsis thaliana."; Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
             Pfam, PF03446; NAD binding 2; 1.
PRINTS, PR0076; 6F0HDRGNASE.
PROSITE; PS00895; 3 HYDROXXISOBUT DH; 1.
SEQUENCE 289 AA; 30691 MW; 3E67002A19706636 CRC64;
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                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                           1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
                                                                                                                                                                                                                                          343 AA.
                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                     (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                            PRT;
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Pfam; PF03446; NAD binding 2; 1.
InterPro; IPR006115; 6PGD NAD
                                                                                  62.5%;
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                                                                                                              23; Conservative
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SEQUENCE 343 AA; 3
                                                                                  Query Match
Best Local Similarity
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                                                                                                              Matches
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Length 343;

Score 123; DB 10; Pred. No. 9.9e-08;

61.5%; 64.7%;

Best Local Similarity

Query Match

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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bai B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
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                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Genomic sequence for Arabidopsis thaliana BAC F1L3 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                           Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 AA.
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  387
                                                                                                                              F1L3.35.
Arabidopsis thaliana (Mouse-ear cress).
                                                      Created)
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  PRT;
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SEQUENCE 387 AA; 41484 MW; 0
                                                (TrEMBLrel. 15, (TrEMBLrel. 15,
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22,
24,
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PRELIMINARY;
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Submitted (FEB-2000)
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Submitted (APR-2000)
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01-OCT-2002 (
01-OCT-2002 (
01-JUN-2003 (
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Q8LQJ7
ID Q8LQJ
AC Q8LQJ
DT 01-OC
DT 01-OC
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Pfam; PF03446; NAD binding 2; 1.
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SO KW DR
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Finding of various plant nuclear proteins using yeast nuclear
transportation trap system - a proteomal approach.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AR24558; AR0726781; -
GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0006464; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.
GO; GO:000698; P:pentose-phosphate shunt; IEA.
GO; GO:0006573; P:valine metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                     Gramene, Q8LQJ7; -. GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA. GO; GO:00084616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA. GO; GO:0006098; P:pentose-phosphate shunt; IEA.
                                                                                                                                                                                                   STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRANIE-CV. Nipponbare;
STRANIE-CV. Nipponbare;
Cooper B., Hutchison D., Park S., Guimil S., Luginbuhl P., Ellero C.,
Goff S., Glazebrook J.;
"Identification of Rice (oryza sativa) Proteins Linked to the Cyclin-
Mediated Regulation of the Cell Cycle.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                     Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein).
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeee, Oryza.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUT-2003 (TrEMBLrel. 25, Last annotation update)
Gamma hydroxybutyrate dehydrogenase-like protein (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                        Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003413; BAB91904.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEGM; PF03446; NAD binding 2; 1.
PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
SEQUENCE 343 AA; 35481 MW; 195ABBEDA048F84D CRC64;
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64.7%; Pred. No. 1.8e-07;
iive 4; Mismatches 8;
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gamma hydroxybutyrate dehydrogenase
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InterPro; IPR006115; 6PGD NAD.
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InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD_NAD.
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Matches 22, Conservative
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                                                                                                                                   NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                       clone:B1151A10."
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                     B1151A10
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084VC8
1D Q84VC
AC Q84VC
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900, G0:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA. G0; G0:0004618; F:phosphoglucopate shunt; IEA. InterPro; IPR006183; 6PGD. ND. InterPro; IPR006183; 6PGD ND. PFGA. PF03446; NAD binding 2; IPR00618; PR007076; 6PGDHDRGNASE.
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                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Dehydrogenase related to 3-hydroxyisobutyrate dehydrogenase, YKWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                            Length 293;
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                                                                                                                            30496 MW; 2362B7AC4EE52038 CRC64;
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Last annotation update)
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ω
                                                                                                                                                                                                                Score 118; DB 10;
Pred. No. 3.7e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GFLGLGIMGKAMAANLLRHGFRVTVWNRTLSKC 36
                                                                                                                                                                                 59.0%; Sco. No. 5... 63.6%; Pred. No. 5... 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFIGTGVMGKGMIKULLKGGYTVHVYNRTKEK 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.
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PRINTS; PRO0076; 6FGDHDRGNASE.
PROSTIE; PRO0095; 3 HYDROXXISOBUT_DH; 1.
Hypothetical protein.
SEQUENCE 293 AA; 30496 MW; 2362B7AC4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                        Local Similarity 63.6
ses 21; Conservative
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SEQUENCE FROM N.A.

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SEQUENCE ATC 35395 / DSM 2834;

MEDLINE=21929760; PubMed=11932334;

MEDLINE=21929760; PubMed=11932334;

MEDLINE=21929760; PubMed=11932334;

MEDLINE=21929760; PubMed=11932334;

MEDLINE=21929760; PubMed=11932334;

MEDLINE M., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Allen N., McKernan K., Talamas J., Tirrell A., Yew., A Linton L., McKernan K., Talamas D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kursycki J.A.,

Medderich R., Ingram-Smith C., Kuertner H.C., Krzycki J.A.,

Melgh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

Metcalf W.W., Birren B.;

The genome of Methanosancian acetivorans reveals extensive metabolic
   GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA. GO; GO:0006098; P:pentose-phosphate shunt; IEA. InterPro; IPR006115; 6FGD NAD. Pfam; PF03446; NAD binding_2; 1. Complete proteome. SEQUENCE 155 AA; 16030 MW; 7FB9B77D3CC771A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and physiological diversity.";
Genome Res. 12:532-542(2002).
EMBL; AR010722; AAM04058.1; -.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
                                                                                                                      Length 155;
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Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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Last annotation update)
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Last annotation update)
                                                                                                                      52.5%; Score 105; DB 16; 59.4%; Pred. No. 9.3e-06;
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Pred. No. 6.2e-05;
5; Mismatches 13;
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InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD NAD.
                                                                                                                                                                                                          3 LGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
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                                                                                                                                                       4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         3-hydroxyisobutyrate dehydrogenase.
MA0614,
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PRINTS; PR00076; 6PGDHDRGNASE.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2003 (TrEMBLrel. 24,
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24,
25.
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                                                                                                                                                       19; Conservative
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                                                                                                                      Query Match
Best Local Similarity
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01-JUN-2003
01-OCT-2003
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Q88UE9;
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                                                                                                                                                                                                                                                   GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0008567; F:nucleic acid binding; IEA.
GO; GO:0004616; F:nucleic acid binding; IEA.
GO; GO:0006608; P:pentose-phosphate shunt; IEA.
GO; GO:0006598; P:pentose-phosphate shunt; IEA.
InterPro; IPR002204; 3hydroxisobut_dh.
                                                         She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Tozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.",
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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Last annotation update)
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Pred. No. 7.3e-06;
7; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
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Rhizobium meliloti (Sinorhizobium meliloti).
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PROSITE; PS00895; 3 HYDROXYISOBUT_DH; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
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(TrEMBLrel. 19, Last seq
(TrEMBLrel. 24, Last anno
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[1]
SEQUENCE FROM N.A.
STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; Pubmed=11427726;
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InterPro; IPR000504; RNA rec mot.
Pfam; PF03446; NAD_binding_2; 1.
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58.8%;
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01-DEC-2001
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292 AA; 31987 MW; 8B04FC5E59A93423 CRC64;
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                                                                      49.58;
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 opportunistic pathogen.",
Nature 406:959-964(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probable dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
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                                                                                                     Best Local Similarity
Matches 18; Conservant
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          SEQUENCE
                                                                      Query Match
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Q911R8
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                                                                                                                                                                                                                                                                                                                                            Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D., Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D., Kliers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M., Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A., Hoffer S.M., Nierop Groot M.N., Kerkhoven R. M., Bron P.A., Ursing B., De Vos W.M., Siezen R.J.;

"Complete genome sequence of Lactobacillus plantarum WCFS1.";

Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).

EMBL; AL935559; CAD64827.1;

GO; GO:0004420; F:3-hydroxymethylglutaryl-CoA reductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. ..; IEA.

GO; GO:0009688; P:biosynthesis, IEA.

GO; GO:0006988; P:pentose-phosphate shunt; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman B., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.,
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                                          HIBD OR LP 2548.
Lactobacillus plantarum.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacceria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Complete proteome.
SROUENCE 286 AA; 30351 MW; AC9E968BD5C222FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31).
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          3-hydroxyisobutyrate dehydrogenase (EC 1:1.1.31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016491; F:oxidoreductase activity; I GO; GO:0004616; F:phosphogluconate dehydroge GO:000000918; P:phosphogluconate dehydroge GO:00000098; P:phosphthesis; IEA. GO; GO:0000098; P:pentose-phosphate shunt; I InterPro; IPR002212; HWG-GoA_red. Pfam; PR03446; NAD binding 2; I. PROSITE; PS00066; HWG-COA_REDUCTASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .-JUN-2003 (TrEMBLrel. 24, Created)
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MEDLINE=22608415; Pubmed=12721630;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=NCIMB 8826 / WCFS1;
MEDLINE=22480296; PubMed=12566566;
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InterPro; IPR006115; 6PGD NAD.
Pfam; PP03446; NAD binding 2; 1
PRINTS; PR00076; 6PGDHDRGNASE.
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Nature 423:87-91(2003)
                                                                                                                                                                                      NCBI_TaxID=1590;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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MEDLINE=22423060; PubMed=12534463;
MELSON R.B., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
                                                                                Gaps
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GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.

GO; GO:0006573; P:valine metabolism; IEA.

InterPro; IPR002204; 3hydroxisobut_dh.

PROSITE; PS00895; 3_HYDROXXISOBUT_DH; 1.
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Pseudomonadaceae; Pseudomonas.
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Score 99; DB 16; Length 292;
Pred. No. 0.00011;
9; Mismatches 11; Indels
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                        GFIGIGWGKSMVYHLMQDGHKVXVVNRTKAKTDSLVQ 46
                                                                                                                                                  1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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49.0%; Score 98; DB 16;
Best Local Similarity 52.9%; Pred. No. 0.00015;
Matches 18; Conservative 7; Mismatches 9;
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EMBL, AP003001, BAB50239.1, -.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T., Nelson K.B., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Heltzapple E.K., Okstead O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C., Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The genome sequence of Bacillus anthracis Ames and comparison to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.0%; Score 96; DB 16; Length 317; 51.4%; Pred. No. 0.00029;
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Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Indels
                                                                                                                                                                                            Dehydrogenase, putative.
BA1842.
Bacillus anthracis (strain Ames).
Bacieria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                    Created)
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        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22608414; PubMed=12721629;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE017029; AAP25747.1; -. TIGR; BA1842; -.
                                                                                                                                                        25,
                                                                    01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           closely related bacteria.";
Nature 423:81-86(2003).
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DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 51.4 ses 18; Conservative
        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                    01-JUN-2003 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Q98GH7
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                                                                                                                                                                                                                                                                "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).

EMBL; ABO16778; AAN66768.1; -...

TIGR; PP1143; -...

ANN66768.1; -...

TIGR; PP1143; -...

TIGR; PP1143; -...

TIGR; PP1145; PP1145; -...

TIGR; PP1145; PP1
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DNA Res. 9:189-197(2002).
EMBL; APO05957; BAC51395.1; -.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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48.0%; Score 96; DB 16; Length 295;
Best Local Similarity 51.5%; Pred. No. 0.00027;
Matches 17; Conservative 6; Mismatches 10; Indels
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Bradyrhizobiaceae; Bradyrhizobium.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD_NAD.
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56.2%;
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Best Local Similarity 56.2<sup>3</sup>
Matches 18; Conservative
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RESULT 21

RESULT 22 Q81535

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RESULT 25

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MEDILNE=91194799; PubMed=8449881;
Fajardo-Cavazos P., Salazar C., Nicholson W.L.;
"Molecular cloning and characterization of the Bacillus subtilis spore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,

Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

Usuda Y., Sugimcin S.;

"The entire genomic sequence of Corynebacterium efficiens YS-314.";

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BMBL, AP005219; BAC18398.1; --

GO, GO:0004616; Fiphosphogluconate dehydrogenase (decarboxyla...;

GO, GO:0006098; P:pentose-phosphate shunt; IEA.
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                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium.
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Pred. No. 0.0011;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative 6-phospho-gluconate dehydrogenase (Fragment).
                                                                                 Last sequence update)
Last annotation update)
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                         490 AA
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                                                                                                                           Putative 6-phosphogluconate dehydrogenase.
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InterPro; IPR006183; 6PGD. C_like.
InterPro; IPR006184; 6PGD BS.
InterPro; IPR006114; 6PGD C.
InterPro; IPR006114; 6PGD C.
InterPro; IPR006115; 6PGD ABD.
Ffam; PP00393; 6PGD; 1.
Ffam; PP00393; 6PGD; 1.
PFam; PP03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
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                                                            01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                 Corynebacterium efficiens.
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                         PRELIMINARY;
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                                                                                                                                                                                                                         NCBI_TaxID=152794;
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                                           Q8FTI1;
                       Q8FT11
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Nat. Biotechnol. 21:526-531(2003).
BMBL; AR005027; BAC69253.1; -.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
GO; GO:0006098; P:pentose-phosphate shunt; IEA.
InterPro; IPR006115; 6PGD NAD.
Pfam; PF03446; NAD_binding_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa U., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                 Length 475;
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                         475 AA; 50478 MW; DDCD80AE38E22DEE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                       7 GLIGLGTMGSNLALNIAEHGHRIAVFNRTRARTDAFVE 44
                                                                                                                                                                                                                                                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                               Score 96; DB 16;
Pred. No. 0.00045;
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InterPro; IPR006183; 6PGJ.
InterPro; IPR006184; 6PGG.
InterPro; IPR0061184; 6PGG.
InterPro; IPR006113; 6PGJ decarbox.
InterPro; IPR006113; 6PGJ decarbox.
InterPro; IPR006115; 6PGJ decarbox.
InterPro; IPR006115; 6PGD NAD.
Pfam; PF03446; NAD binding 2; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
TICRFAMS; TICRD0893; gnd; 1.
COMDIETE; PS00461; 6PGD; 1.
COMDIETE PROTOCEOME.
SEQUENCE 475 AA; 50478 MW; DDCD80.
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Best Local Similarity 42.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q82MW0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OB2MW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q82MW0
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SEQUENCE FROM N.A.

MEDLINE=22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

MEDLINE-22827954; PubMed=12910271;

MARTIS D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Corden-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Achtman M., Atkin R., Baker S., Sanders M., Saunders D., Seger K.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seger K.,

Sharp S., Simmonda M., Skelton J., Squares R., Squares S., Stevens K.,

W. Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"Not Comparative analysis and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Goldsmith A.D., Lee J.M., Quach H.L., Tang C.C., Toriumi M., Yu G.,
                                                                                              Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.0%; Score 92; DB 16; Length 302; 58.1%; Pred. No. 0.00092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 AA; 31371 MW; B9696B7BAD09CA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein (Putative dehydrogenase) F19815.150 OR AT4G29120.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLGLGVMGLPMAGHLARAGHQVTVYNRTAAK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Genet. 35:32-40(2003).
EMBL; BX640434; CAE39062.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dery Match
Set Local Similarity 58.1",
Best Local 18; Conservative
                                                                     Bordetella parapertussis.
Bacteria; Proteobacteria; B
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                        Putative oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9SZE1
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                                                                                                                    . .; IEA.
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Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

Cardeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pertussis,

Bordetella parapertussis and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                           GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .;
GO; GO:00066098; P:pentose-phosphate shunt; IEA.
GO; GO:0006573; P:valine metabolism; IEA.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006115; 6PGD_NAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
photoproduct lyase (spl) gene, which is involved in repair of radiation-induced DNA damage during spore germination."; J. Bacteriol. 175:1735-1744 (1993).

EMBL: X97385; CAA66053.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.0%; Score 92; DB 16; Length 301; 58.1%; Pred. No. 0.00091;
                                                                                                                                                                                                                                                                                                                                                           Score 92; DB 2; Length 43;
Pred. No. 0.00012;
6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 AA; 31326 MW; 91AC4FBF73F6925F CRC64;
                                                                                                                                                                                                                                                                                                              43 AA; 4797 MW; 4E9F29CDCB64945B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFIGLGVMGKSMASHILNDGHPVLVYTRTKEK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLGLGVMGLPMAGHLARAGHQVTVYNRTAAK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 AA
                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                      Pfam; PF03446; NAD binding 2; 1.
PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX640449; CAE34588.1; -.
                                                                                                                                                                                                                                                                                                                                                              46.0%;
                                                                                                                                                                                                                                                                                                                                                                                      53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alcaligenaceae, Bordetella.
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=RB50 / ATCC BAA-588;
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 53.13
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                           43
                                                                                                                                                                                                                                                                                                                 SEQUENCE
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O7WFP7;

Q7WFP7

RESULT 27

Q7W489;

Q7W489

RESULT 28

Q7W489

Best Loca Matches

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Gaps

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Search completed: September 16, 2004, 07:45:56
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            RRA
RRA
RRI
RRI
DR CDR
SQ
SQ
SQ
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                                                                                                                                                                                                                                            Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chenk R.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlın-Neumann G.,
Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
Theologis A.; Shinozaki K., Davis R.W., Ecker J.R.,
L. Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL078470; CAB43926.1; -
BEBL; AL16574; CAB79670.1; -
BEBL; AV062952; AAL33784.1; -
BR PIR; T08967; T08967.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA. GO:0008152; P:metabolism; IEA.
Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Sekim M., Shinn P., Southwick A., Shinnzaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length cDNA of gene AT4229120 (GI:7269810)."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEPLINE-2202145; PubMed=12024217; MEDLINE-22022145; PubMed=12024217; da Silva A.C.R., Ferro U.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., Camarotte G., Cannaravan F., Cardozo J., Chambergo F., Ciaphia L.P., Caracilli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira R.C.C., Ferro M.I.T., Formighleri B.F., Franco M.C., Greggio C.C., Gruber A., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali B.C., Machado M.A., Madeira A.M.B.N., Matrinez-Rossi N.M., Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.0%; Score 92; DB 10; Length 334; 45.9%; Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00498; TYROSINASE_2; 1.
Hypothetical protein.
SEQUENCE 334 Aa; 35371 MW; EC0038096DB836BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 GWIGTGVWGRSWCGHLIKAGYTVTVFNRTISKAQTLI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0006098; P:pentose-phosphate shunt; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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InterPro; IPR006115; 6PGD NAD.
InterPro; IPR002227; TyroSinase.
Pfam; PF03446; NAD_binding_2; 1.
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Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P., "Comparison of the genomes of two Xanthomonas pathogens with differing
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EMBL; AB011657; AAM35214.1; -.
G0; G0:008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
G0; G0:0006573; P:valine metabolism; IEA.
InterPro; IPR002204; 3hydroxisobut dh.
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Secreted protein; nutritional source; cell proliferation activity; cell differentiation activity; immune stimulant; tissue growth activator; haematopoiesis regulator; anti-inflammatory; tumour invasion suppressor;
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Y;
                                                                                                                                                                                                                                                                                                                                                         cell proliferative disorder; atherosclerosis; dirhosis; hepatitis; AIDS; cancer; developmental disorder; renal tubular acidosis; anaemia; asthma; mental retardation; neurological disorder; Alzheimer's disease; epilepsy; Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy; Crohn's disease; transgenic animal; animal model.
Aab 92800 Human pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid-associated proteins and polynucleotides, useful for diagnosing, treating or preventing cell proliferative (e.g. cancer), neurological (e.g. epilepsy or Parkinson's disease), or autoimmune disorders (e.g. AIDS).
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Zebarjadian Y, Li
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Arvizu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forsythe
Ramkumar J, Griffin JA, Yang J, Sanjanwala MM, Baughn MR;
Borowsky ML, Yao MG, Walia NK, Bandman O, Lal PG, Becha S
Richardson TW, Elliott VS, Luo W, Tang YT, Zebarjadian Y,
                                                                                                                                                                                                                                                                                                      Human nucleic acid-associated protein (NAAP) - SEQ ID No 12
                                                                                  ALIGNMENTS
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06-UUL-2001;
15-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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97US-00989232

11-DEC-1997;

(GEMY ) GENETICS INST INC.

Sequence 553

480 480 540 540

Human AQ73_3 protein sequence SEQ ID 137.

(first entry)

07-JUN-2001

AAB90720;

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Score 2811; DB 2;
Pred. No. 5.8e-250;
       Racie LA,
                                                                                                                                              0; Mismatches
                                                   Claim 15; Page 66-67; 108pp; English.
      Lavallie ER,
                                                                                                                                   98.1%;
98.7%;
           V, Agostino MJ;
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                                                                                                                                             Matches 546; Conservative
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      Mccoy JM,
                     WPI; 1998-362424/31.
                                                                                                                                       Local Similarity
                          N-PSDB; AAV44859
                                                                                                                        Sequence 547 AA;
          Spaulding
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                                                                                                                                  Query Match
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AAB90720 standard; protein; 547 AA.

AAB90720 ID AAB9 RESULT 3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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|-----EGARLGRIPAEVUSTCDITFACVSDFRAAKDLVLGPSGVLQGIRPGKCYUDM 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STVDADIVIELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM 414
                                                                                                                                                            This sequence is secreted protein, encoded by a polynucleotide of the invention. The DNA was isolated from a human adult ovary CDNA library, and is designated clone AQ73 3. The DNA sequences and encoded polypeptides can be used as nutritional sources or supplements, or may immune stimulating or suppressing activity, haematopoiesis regulating activity, receptor/ligand activity, nuti-inflammatory activity, activity, activity, clemostatic/chemokinetic activity, cadherin/tumour invasion suppressor activity, tissue growth activity, tumour inhibition activity or other activity, tissue growth activity,
                                                                                      New isolated polynucleotides - obtained from human adult testis, human adult ovary, human adult brain and human adult heart cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRP
                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSGDEKRKLSLSEGKVKKKMMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKTSFFLGEVGNAARMMLIVNMVQGSFMATIAEGLTLAQVTGQSQTLLDILNQGQLASI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQS
          Treacy M;
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                                                                                                                                                                                                                                                                                                                                                                      Length 547;
         Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Proteins, their agonists and/or natagonists exhibit haematopoises; proteins, their agonists and/or natagonists exhibit haematopoises; regulating activity, issue growth activity, activin/inhibin activity, rememeratiof/chemokinetic activity, haemostatic and thrombolytic activity; receptor/ligand activity; anti-inflammatory activity, haematopoises; activity; cadherin/tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAF98490 - AAF98572 which are specific for the cDNA clones encoding the secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA clones represented in AAF98374 - AAF98489 encode secreted proteins AAB90667 - AAB90750. The cDNA clones are isolated from various tissue types, and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The polypeptides and nucleic acids may be used as nutrients or to modulate cytokine and cell proliferation/differentiation activity and may also be involved in modulation of the immune system. The cDNA sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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Human; secreted protein; nutrient; cytokine modulator; proliferation; differentiation; immune system modulator; tissue growth; chemotactic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; haematopoiesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acids encoding polypeptides, useful for modulating e cytokine and cell proliferation/differentiation activity, the immune system and hematopoiesis regulating activity.
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Pred. No. 5.8e-250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bowman MR,
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98.7%;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                      534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; neoplastic disease associated polypeptide; cancer; hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic.
                                                                                                                                                                                                                                                         FLDOKCONILOGNFKPDFYLKYIOKDLRLAIALGDAVNHPTPWAAAANEVYKRAKALDOS
                                                                                                                                                                                                                                                                          475 FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTFWAAAANEVYKRAKALDQS
                     ICEEETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTA
                                                                            Novel human neoplastic disease associated polypeptide #123
                                                                                                                                                                                                                                                                                                                                                                                                                              AAU21690 standard; protein; 550 AA
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14-AUG-2000;
14-AUG-2000;
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AAU21690
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Novel polypeptides and polynucleotides useful as diagnostic reagents to
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2000US-0246609P
2000US-0246609P
2000US-0246610P
2000US-0246611P
2000US-0246611P
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2000US-0249244P
2000US-0249244F
2000US-024924F
2000US-0249265P
2000US-0249297P
2000US-0249297P
2000US-0249297P
2000US-0250160P
2000US-0250160P
2000US-0250160P
2000US-0250160P
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2000US-0249215P.
2000US-0249216P.
2000US-0249216P.
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2000US-0251869P.
2000US-0251989P.
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2000US-0249209P.
2000US-0249210P.
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2000US-0249212P.
2000US-0249213P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-465558/50
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                                                                          08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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01-DEC-2000;
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05-DEC-2000;
                                         08-NOV-2000;
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The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS3467-AAS35050) and DNA considers encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative of disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem clinks and in the diagnosis, childhood cerebellar astrocytoma, or Hoddxin's lymphoma). The sequences of the invention may also be useful of isorders, muscular disorders, immune system clisorders, pulmonary disorders, reproductive disorders, immune system disorders, pulmonary disorders, reproductive disorders and renal disorders. The polymucleotide sequences of the invention are also useful clisorders. The polymucleotide sequences of the invention are also useful clisorate therapy. AAUSIS68-AAUS1851 represent the novel human neoplastic clisanse associated polypeptides of the invention. Note: The sequence data contained in electronic form part of the printed specification, but was the wide in though published per sequences. diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis

US2003082758-A1.

Sequence 550 AA;

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                                                                                                                                    64 HAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSG 123
                                                                                                                                                                                                       DEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKDLTI 183
                                                                                                                                                                   67 HAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 ÇKCÇNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAANEVYKRAKALDQSDND 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neoplastic disease-associated polypeptide; gene therapy; hyperproliferative disease; cancer; autoimmune disorder; diabetes; rheumatorid arthritis; systemic lupus erythematosus; multiple sclerosis; autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder; haematologic disorder; anaemia; thrombocytopaenia; allergic reaction; sathma; eczema; inflammatory disorder; ischaemia-reperfusion injury; inflammatory bowel disease; crbm's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; renal disorder; acute glomerulonephritis; end-stage renal disease; cardiovascular disorder; atherosclerosis; myocarditis; infectious disease; AlDS; cachexia; anorexia; wound healing; epithelial cell proliferation; Human.
                                                                    VSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPY
                                                                                                  7 VSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPY
                                                                                                                                                                                                                          EETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKC
                                                                                                                                                                                                                                                                                                                                                                                                            304 DLFIQEGARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                   306 -----BGARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFFLGEVGNAAKWMLIVNMVQGSFMATIAEGLTLAHVTGOSQQTLLDILNQGQLASIFLD
                                                                                                                                                                                                                                                                        PESSTVKGMMAGPWAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLKICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 DADIVTBLAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYBDCSSCFQAMGKT
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 DADTVIELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCRQAMGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 SFFLGEVGNAAKOMLIVNMVQGSFMATIAEGLTLAQVTGQSQQTLLDILNQGQLASIFLD
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          Length 550;
                                          1; Indels
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       Score 2798; DB 4;
Pred. No. 9.3e-249;
0; Mismatches 1;
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   97.68;
Query Match
Best Local Similarity 98.7
Matches 543; Conservative
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31-JAN-2000; 2000US-0179065P.

24-FEB-2000; 2000US-018605BP.

22-MAR-2000; 2000US-018605BP.

16-MAR-2000; 2000US-018605BP.

16-MAR-2000; 2000US-018605BP.

16-MAY-2000; 2000US-0190076P.

19-MAY-2000; 2000US-01913P.

19-MAY-2000; 2000US-020515P.

19-MAY-2000; 2000US-020515P.

26-JUL-2000; 2000US-021864P.

11-JUL-2000; 2000US-021864P.

11-JUL-2000; 2000US-021864P.

11-JUL-2000; 200US-021864P.

11-JUL-2000; 200US-021868P.

11-JUL-2000; 200US-021868P.

11-JUL-2000; 200US-021868P.

11-JUL-2000; 200US-022184P.

14-AUG-2000; 200US-022514P.

14-AUG-2000; 200US-022914P.

14-AUG-2000; 200US-022914P.

14-AUG-2000; 200US-022914P.

14-SEP-2000; 200US-022914P.

14-SEP-2000; 200US-02314P.

14-SEP-2000; 
                             2002US-00103313
                             22-MAR-2002;
01-MAY-2003
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29-SEP-2000; 2000US-025369P: 02-OCT-2000; 2000US-023703PD: 02-OCT-2000; 2000US-023993PD: 02-OCT-2000; 2000US-0240960PD: 02-OCT-2000; 2000US-024186PD: 02-OCT-2000; 2000US-024186PD: 02-OCT-2000; 2000US-024186PD: 02-OCT-2000; 2000US-024186PD: 02-OCT-2000; 2000US-024186PD: 02-OCT-2000; 2000US-024186PD: 02-OCT-2000; 2000US-024647PD: 03-NOV-2000; 2000US-024647PD: 03-NOV-2000; 2000US-024647PD: 03-NOV-2000; 2000US-024647PD: 03-NOV-2000; 2000US-024647PD: 03-NOV-2000; 2000US-024652PD: 03-NOV-2000; 2000US-024651PD: 03-NOV-2000; 2000US-024652PD: 03-NOV-2000; 2000US-024921PD: 17-NOV-2000; 2000US-0224921PD: 17-NOV-2000; 2000US-024921PD: 17-NO

29-SEP-2000; 2
29-SEP-2000; 2
22-OCT-2000; 2
02-OCT-2000; 2
02-OCT-2000; 2
13-OCT-2000; 2
13-OCT-2000; 2
20-OCT-2000; 2
20-OCT

Barash SC;

SM, Ruben

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(HUMA-) HUMAN GENOME

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The invention relates to one of 238 disclosed human neoplastic disease—
associated polypeptides encoded by 171 disclosed cDNA sequences
(including their domains, epitopes, full-length proteins, allelic variants
or species homologues). Also included are there encoding nucleic acids, a
recombinant vector comprising the nucleic acid, a recombinant host cell
comprising the nucleic acid (expressing the protein), an isolated
antibody that binds specifically to the isolated polypeptide, preventing,
condition or a susceptibility to a pathological condition in a subject,
in a biological assay, and the gene corresponding to the CDNA sequence.
Condition or a susceptibility to a pathological condition in a subject,
in a biological assay, and the gene corresponding to the CDNA sequence.
Conditions a polypeptides, polynucleotides and antibodies are useful for
the polypeptides, polynucleotides and antibodies are useful for
ameliorating medical conditions such as hyperproliferative diseases or
ameliorating medical conditions such as hyperproliferative diseases
conference in a unique systemic lupus exprhematosus, multiple sclerosis, autoimmune thyroiditis
or haemolytic anaemia), haematopoietic or heematologic disorders (e.g.
canaemia or thrombocytopaenia), allergic reactions including asthma or
eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
                                                                                    New isolated human neoplastic disease-associated polypeptides and polymucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 417; 302pp; English.
      WPI; 2003-786918/74.
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Gaps 9 Indels 97.6%; Score 2798; DB 7; 98.7%; Pred. No. 9.3e-249; 0; Mismatches Query Match Best Local Similarity 98.7 Matches 543; Conservative

123 186 243 305 363 DADIVIELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKT 423 63 99 483 SFFLGEVGNAAKVMLITUNMVQGSFNATIAEGLTLAQVTGQSQQTLLDILNQGQLASIFLD 480 7 VSLRLGDLVWGKLGRYPPWPGKLVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPY HAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRNSSEERSRPNSG PESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHPLLSQTEKPAVCYQAITKKLKICE EETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKC ----EGARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTV 4 VSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKÇFFVKFFGTEDHAWIKVEQLKPY 124 DEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKDLTI EETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNKTAEK-DLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTV SFFLGEVGNAAKMMLIVNMVQGSFMATIABGLTLAHVTGQSQQTLLDIINQGQLASIFLD QKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDND |||||||||| 541 MSAVYRAYIH 550 MSAVYRAYIH 553 244 304 306 364 361 124 421 181 544 184 ò à g ò g

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The invention relates to human enzyme (ENZM) polypeptides and their corresponding polynucleotides. ENZM sequences are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional ENZM. The disorders include immune disorders (anaemia, allergy or asthma), infectious disorders (viral, fungal, parasitic or protozoal infection), immune deficiencies (acquired immune deficiencies (acquired immune deficiencies (acquired immune deficiencies (acquired immune deficiencies), reproductive disorders (infertility or impotence), cardiovascular disorders (atherosclerosis or myocardial infarction), eye disorders and cell proliferative disorders (cancer). ENZM DNA is useful in gene therapy. The
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                                                                                                                                                                                   Human; enzyme; ENZM; immune disorder; infection; myocardial infarction; gene therapy; anaemia; acquired immune deficiency syndrome; infection; reproductive disorder: cardiovascular; eye; cell proliferation; cancer; AIDS; allergy; asthma; Addison's disease; diabetes; goitre; impotence; infertility; atherosclerosis; metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human enzyme (ENZM) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
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Tran UK, Kable AE, Richardson TW, Emerling BM, Lindquist EA;
Baughn MR, Hafalia AJA, Jin P, Swarnakar A, Li JX, Marquis,
Lee S, Gorvad AE, Sprague WW, Becha SD, Elliott VS;
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85.2%; Pred. No. 8.1e-212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overexpression of ENZM e.g. cancer.
                                      AAE38240 standard; protein; 472
                                                                                                                                                Human enzyme (ENZM) protein #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                            14-DEC-2001; 2001US-0340357P.
20-DEC-2001; 2001US-0342962P.
21-DEC-2001; 2001US-0343558P.
22-JAN-2002; 2002US-0351107P.
                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-2002; 2002WO-US040161.
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                                                                                                            (first entry)
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Best Local Similarity 85.2°
Matches 471, Conservative
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                                                                       AAE38240;
RESULT 6
AAE38240
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2000US-0236802P.
2000US-023703P.
2000US-0237038P.
2000US-0237039P.
2000US-0237040P.
2000US-0237040P.
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2000US-0240960P
2000US-0241221P.
2000US-0241785P.
2000US-0241786P.
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2000US-0241808P.
2000US-0241809F.
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2000US-0230437P.
2000US-0231242P.
2000US-0231243P.
2000US-0231243P.
2000US-023143P.
2000US-0231444P.
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New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions

Claim 11; SEQ ID NO 507; 753pp; English.

The invention relates to novel isolated nucleic acid molecules (I) encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with sequences may also be used as DNA probes in diagnostic assays (e.g. sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in

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(agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies can activity of (II). The anti-(II) antibodies may also be used to down regulate expression and activity of (II). The anti-(II) antibodies may also be used as diagnostic agents for detecting the presence of (II) in samples (e.g. by enzyme linked immunosorbant assay (ELISA). The disorders include for example: immune/autoimmune diseases (e.g. HIV) (human immunodeficiency virus) infections, anaemia, rheumatoind arthritis and multiple sclerosis), cancers and hyperroliferative disorders (e.g. Cancers and hyperroliferative disorders (e.g. Parkinson's disease, and charact-Marie-Tooth disease), cardio-/
Caerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and thrombosis), infections caused by bacteria, viruses and fungia and ocular disorders (e.g. corneal infections). (I) and (II), agonists, antagonists and antibodies can also be used to promote wound healing, maintain organs before transplantation, and support cell culture of primary tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VSLXLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPY
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the production of antibodies and in assays to identify modulators
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2000US-024121P2000US-0241785P2000US-0241787P2000US-0241787P2000US-0241787P2000US-02441787P2000US-0244617P2000US-0246475P2000US-0246478P2000US-0246478P2000US-0246478P2000US-0246478P2000US-0246478P2000US-0246523P2000US-0246523P2000US-0246523P2000US-0246523P2000US-0246523P2000US-0246513P2000US-0246513P2000US-0246513P2000US-0246513P2000US-0246513P2000US-0246513P2000US-0246513P2000US-0246513P2000US-0246513P2000US-0249209P2000US-0249213P2000US-0249214P2000US-0249214P2000US-0249214P2000US-0249214P2000US-024921P2000US-0249214P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-0249218P2000US-025931P2000US-025931P2000US-025938P2000US-025988P2000US-0251868P-2001US-0259678P 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 01-DEC-2000; 01-DEC-2000; 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 20-OCT-2000; 20-OC 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; -NOV-2000; -NOV-2000; -NOV-2000; 17-NOV-2000; 17-NOV-2000; 05-JAN-2001; NOV-2000; 17-NOV-2000; 17-NOV-2000; L7-NOV-2000; 11-DEC-2000 

(HUMA-) HUMAN GENOME

SM Ruben Barash SC, Rosen CA,

WPI; 2001-465558/50. N-PSDB; AAS35012.

Novel polypeptides and polymucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis.

Claim 11; SEQ ID NO 540; 687pp; English

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and CDNA (AAS34767-AAS35050) and DNA

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are useful in the diagnosis, treatment, prevention and/or proposis of disorders involving neoplastic disease such as hyperproliferative disorders involving neoplastic disease such as hyperproliferative glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, immune system disorders, pulmonary disorders, reproductive disorders, gastrointestinal disorders. pulmonary disorders, reproductive disorders and renal in gene therapy. Adults68-AAU1881 represent the novel human neoplastic disease associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences]
                                                                                                                                                                                                                                                                       0
  sequences encoding for these polypeptides. The sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                     61 HAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neoplastic disease-associated polypeptide; gene therapy; thyperproliferative disease; cancer; autoimmune disorder; diabetes; rheumatorid arthritis; systemic lupus erythematosus; multiple sclerosis; autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder; haematologic disorder; anaemia; thrombocytopaenia; allergic reaction; asthma; eczema; inflammatory disorder; ischaemia-repertusion injury; inflammatory bowel disease; crohn's disease; neurodegenerative disorder; acute glomenlonephritis; end-stage renal disease; cand disorder; cardicoascular disorder; atherosclerosis; myocarditis; infectious disease; AIDS; canchexia; myocarditis; infectious disease; AIDS; canchexia; mound healing; epithelial cell proliferation; Human.
                                                                                                                                                                                                                                                                                        4 VSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVBQLKPY
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Matches 267; Conservative
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11-JUL-2000; 2000US-0217496P.
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02-MAR-2000;
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19-MAY-2000;
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02-OCT-2000; 2000US-0237040P.

13-OCT-2000; 2000US-0237040P.

20-OCT-2000; 2000US-023935P.

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20-OCT-2000; 2000US-0241231P.

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20-OCT-2000; 2000US-024182FP.

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20-OCT-2000; 2000US-024677P.

08-NOV-2000; 2000US-024647FP.

08-NOV-2000; 2000US-024647FP.

08-NOV-2000; 2000US-024652FP.

08-NOV-2000; 2000US-024653PP.

08-NOV-2000; 2000US-024653PP.

08-NOV-2000; 2000US-024653PP.
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2000US-0237040P.
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2000US-0239937P.
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17-NOV-2000; 2000US-0249208P.
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17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249210P.
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2000US-0249216P.
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17-NOV-2000; 2000US-0249299F.
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01-DEC-2000; 2000US-0250391P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-025130P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025149F.
08-DEC-2000; 2000US-025149P.
08-DEC-2000; 2000US-0251866P.
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2000US-0249265P.
2000US-0249297P.
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Barash SC; Ruben SM, WPI; 2003-786918/74. N-PSDB; ADC46170. Rosen CA,

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The invention relates to one of 238 disclosed human neoplastic disease—
associated polypeptides encoded by 171 disclosed cDNA sequences
considered polypeptides encoded by 171 disclosed cDNA sequences
(including their domains, epitopes, full-length proteins, allellic variants
or species homologues). Also included are there encoding nucleic acids, a
comprising the nucleic acid (expressing the protein), an isolated
continuous binds specifically to the isolated polypeptide, preventing,
treating or ameliorating a medical condition, diagnosing a pathological
condition or a susceptibility to a pathological condition in a subject,
condition or a binding partner to the polypeptide, identifying an activity
in a biological assay, and the gene corresponding to the cDNA sequence.
Conditions preventing, diagnosing, prognosticating, treating or
cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
contracting medical conditions such as hyperproliferative diseases or
cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
contracting preventing, medical solutions such as hyperproliferative diseases or
cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
contracting or expensions, multiple sclerosis, autoimmune thyroiditis
correlations thrombocytopaenia), haematopologic disorders (e.g.
cor haemolytic anaemia), haematopologic reactions including asthma or
correma, inflammatory disorders (e.g. ischaemia-reperfusion injury,
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New isolated human neoplastic disease-associated polypeptides and polymucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
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                                                                                                              Claim 11; SEQ ID NO 540; 302pp; English
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Best Local Similarity 99.33
Matches 267; Conservative
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DNA encoding human-derived growth factor polypeptide - useful to promote wound healing as result of burns or ulcers.
                                                                                                                                                                                                                                                                            Human hepatoma-derived growth factor-2 (HDGF-2) (AAW09404) shows 23% identity and 61% similarity over a 201-amino acid stretch to human HDGF, a mitogen for fibroblasts. Its amino acid sequence was deduced from a cDNA clone (AAT4750) isolated from a human umbilical vein endothelial tissue cDNA library. Recombinant HDGF-2 can be produced in transformed host (e.g. E. coli, Sf9, COS) celle. It is useful in stimulating tissue repair and tissue growth and can also be used to produce antibodies and to screen for antagonists that retard tumour growth and reduce scarring
                                                                                                                                                                                                                                             Claim 7; Fig 2; 54pp; English
                   95WO-US006731
                                                      (HUMA-) HUMAN GENOME SCI
                                                                                            Rosen CA
                                                                                                                               WPI; 1997-043108/04.
N-PSDB; AAT47520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 249 AA;
                   05-JUN-1995;
                                                                                            Kunsch CA,
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181 LIIPESSIVKGMMAGPMAAFKWQPIASEPVKDADPHFHHFLLSQIEKPAVCYQAITKKLK 240 1 MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL MAAVSLRLGDLVWGKLGRYPPWGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRP LTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLK KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRP NSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD 0; Gaps 45.0%; Score 1291; DB 2; Length 249; 99.6%; Pred. No. 3e-110; Live 1; Mismatches 0; Indels 243; Conservative Local Similarity ICEE 244 241 ICED 244 61 121 121 181 Query Match 241 Matches g ð g δ qq g ò 8

120 120

240

Human; hepatoma-derived growth factor-2; HDGF-2; vasotropic; vulnerary; antinflammatory; gene therapy; vascular endothelial cell growth; re-vascularisation; ischaemic tissue; thrombosis; arteriosclerosis; cardiovascular condition; mesodermal induction; limb regeneration; nound healing; injury; burn; surgery; ulcer; neuronal growth; neuronal damage; neuronal growth; neuronal damage; neuronal growth; changer; ulcer; neuronal growth; neuronal damage; parkinson's disease; ATDS-related complex; chondrocyte growth; bone regeneration; periodontal regeneration; tissue transplant; bone graft; skin aging; sunburn; keratinocyte growth; hair loss; hair-forming cell activation; melanocyte growth; haematopoietic cell growth; haematopoietic cell differentiation; Human hepatoma-derived growth factor 2 (HDGF-2). ABU09982 standard; protein; 249 AA. (first entry) 30-JUL-2003 ABU09982; RESULT 11 ABU09982 

61 KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRP

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The invention describes a polypeptide (I) having a deduced amino acid sequence of human hepatoma-derived growth factor-2 (HDGF-2) polypeptide sequence of 249 amino acids (G2) as given in the specification, or its fragments analogues or derivatives. (I) is useful for stimulating vascular endothelial cell growth, and thus is employed in treatment for stimulating re-vascularisation of ischaemic tissues due to various conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; stimulating mesolerosis, and other cardiovascular conditions; stimulating meaning in wounds due to injuries, burns, suggery, and ulcers, stimulating our preventing neuronal damages occuring in certain children, suggery, and ulcers, stimulating occuring in certain curvonal disorders or neuron-degenerative conditions such as Alzheimer's disease, parkinson's disease, and AIDS-related complex; stimulating changed conditions such as Alzheimer's disease, parkinson's disease, and AIDS-related complex; stimulating changed cranging due to sunburn by stimulating benefit or proventing melanocyte growth; stimulating prowth and differentiation of haemacopoietic cells of sud bone marrow cells; maintaining organs before transplantation; and inducing tissue to mesolustic for inhibiting the cell growth and therefore are useful for inhibiting the cell growth and therefore are useful for inhibiting about and normal cells and therefore are useful for inhibiting about and intumning and crissues, and therefore are useful for inhibiting about and therefore are useful for inhibiting the cell growth and and normal cells and contained and normal cells and contained therefore are useful for preventing about and normal cells and and normal cells and contained and normal cells and cells and normal cells and normal contained and normal cells and cells and normal contained and normal cells and n
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     organ transplantation; mesodermal tissue; cell growth;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and proliferation e.g. in tumour formation or growth; preventing hypervascular diseases and preventing the proliferation of epithelial
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                    cell proliferation, tumour, hypervascular disease; epithelial lens cell proliferation; extracapsular cataract surgery; restenosis; balloon angioplasty; inflammation; scar tissue.
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oo 6%; Pred. No. 3e-110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preventing hair loss.
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   180
                                                                                                                                                                                                                                       Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina; rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; opthchalmological; cytostatic; Alzeimer's disease; Parkinson's disease; human; cancer; multiple sclerosis; cancer; hyperproliferative disorder; infection; Gaucher's disease; neurological disease; cerebrovascular disorder; thrombosis; wound healing.
             NSGDEKRKLSLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD
                                                                                                                                                                                                                          Human secreted protein, Seg ID No 545
                                                                                                                                                                 AAU20553 standard; protein; 260 AA
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2000US-0184664P.
2000US-0189874P.
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2000US-020467P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel isolated nucleic acid molecules (I) encoding human secreted proteins (II) (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 545; 753pp; English.
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2000US-0249245P
2000US-0249264P
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Score 1291; DB 4; Length 260; Pred. No. 3.2e-110;

45.0%;

Query Match Best Local Similarity

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                                                                                                                   121 NSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD 180
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                                                                    61 KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEBRSRP 120
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                                            MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL 71
                      1 MAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
                                                                                                                                                                                                                                                                                                                                                                                           Human; neoplastic disease associated polypeptide; cancer; hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; reproductive disorder; pastroincestinal disorder; pulmonary disorder; ardiovascular disorder; renal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic.
                                                                                                                                                                                                                                                                                                                                                                      Novel human neoplastic disease associated polypeptide #180.
   0; Indels
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The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA sequences encoding for these polypeptides. The sequences of the invention sequences encoding for these polypeptides. The sequences of the invention consists of are useful in the diagnosis. Ireatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders involving neoplastic disease such as hyperproliferative concer, childhood cerebellar astrocytoma, or prognomia, adult liver cancer, childhood cerebellar astrocytoma, or concert, adult liver cancer, childhood cerebellar astrocytoma, or concert, such as neural disorders, immune system for treating other disorders such as neural disorders, immune system cisorders, muscular disorders, reproductive disorders, immune system disorders, disorders, reproductive disorders and renal disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAU21568-AAU21851 represent the novel human neoplastic consenses associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides and polynuclectides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis
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                                                                              2000US-0249207P.
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Length 260;

Score 1291; DB 4; Pred. No. 3.2e-110;

45.0%;

Query Match Best Local Similarity

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                                   Neoplastic disease-associated polypeptide; gene therapy; hyperproliferative disease; cancer; autoimmune disorder; diabetes; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder; haematologic disorder; anaemia; thrombocytopaenia; allergic reaction; sthma; eczema; inflammatory disorder; ischemia-reperfusion injury; inflammatory bowel disease; crohn's disease; renzodegenerative disorder; alzetimer's disease; parkinson's disease; renal disorder; date glomerulonephritis; end-stage renal disease; cancerdisorder; atherosclerosis; myocarditis; infectious disease, allosi, cancerdisorder, atherosclerosis; myocarditis; end-stage renal disease; allosi, cancerdisorder, allosi, cancerdisorder, allosi, anorexia; wound healing; epithelial cell proliferation; Human.
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  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human neoplastic disease-associated polypeptides and polymucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
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08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-024653P.
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05-DEC-2000; 2000US-025193P.
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05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-0251479P.
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08-DEC-2000; 2000US-0251869P.
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ameliorating medical conditions such as hyperproliferative diseases or cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic anaemia), haematopoietic or haematologic disorders (e.g. anaemia or thrombocytopaenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
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99.6%; Pred. No. 3.2e-110;
tive 1; Mismatches 0;
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24-FEB-2000; 2000US-0184664P.
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Best Local Similarity 99.6
Matches 243; Conservative
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Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465558/50. N-PSDB; AAS34789 Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis.

Claim 11; SEQ ID NO 317; 687pp; English.

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders involving neoplastic disease such as hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune system disorders, pulmonary disorders, cardiovascular disorders and renal disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAU21861 represent the novel human neoplastic

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                                                                                              14-AUG-2000;
disease associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                     TIPESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFILISQTEKPAVCYQAITKKLKI 241
                                                                                                                                                                                                                                                                     haematologic disorder; anaemis; thrombocytopenia; allergic reaction; asthma; eczema; inflammatory disorder; ischaemia.reperfusion injury; inflammatory bowel disease; crohn's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; renal disorder; acute glomerulonephritis; end-stage renal disease; acardiovascular disorder; atherosclerosis; myocarditis; infectious disease; AlDS; cachexia, anorexia, wound healing; epithelial cell proliferation; Human.
                                                                                                                                                                             PYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRNSSEERSRPN 121
                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neoplastic disease-associated polypeptide; gene therapy; hyperproliferative disease; cancer; autoimmune disorder; diabetes; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder;
                                                                                                                                                                                                          SGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKDL
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                                                                             44.9%; Score 1286; DB 4;
99.6%; Pred. No. 8.7e-110;
iive 1; Mismatches 0;
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2000US-0180628P.
2000US-0184564P.
2000US-0184350P.
2000US-0189874P.
2000US-0199076P.
2000US-0198123P.
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2000US-020551SP.
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                                                                                                      Matches 242; Conservative
                                                                                  Query Match
Best Local Similarity
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                                                            Sequence 250 AA;
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24-FEB-2000;
02-MAR-2000;
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07-JUN-2000;
28-JUN-2000;
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08-NOV-2000
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New isolated human neoplastic disease-associated polypeptides and polynucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's Rosen CA, Ruben SM, Barash SC; WPI; 2003-786918/74. N-PSDB; ADC45947.

Claim 11; SEQ ID NO 317; 302pp; English.

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The invention relates to one of 238 disclosed human neoplastic disease-associated polypeptides encoded by 171 disclosed cDNA sequences (including their domains, epitopes, full-length proteins, allelic variants or species homologues). Also included are there encoding nucleic acids, a
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Comprising the mucleic acid (expressing the protein), an isolated antibody that binds specifically to the isolated polypeptide, preventing antibody that binds specifically to the isolated polypeptide, preventing, or mateliorating a medical condition, diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, identifying a binding partner to the polypeptide, identifying an activity or a pathological condition in a biological assay, and the gene corresponding to the CDNA sequence. The polypeptides, polyputleotides and antibodies are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions such as hyperproliferative diseases or cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis or haemalytic anaemia), haemacopoietic or haematologic disorders (e.g. canemia or thrombocytopaenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 PYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPN 122
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 recombinant vector comprising the nucleic acid, a recombinant host cell
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                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                   Length 250;
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99.6%; Pred. No. 8.7e-110;
ive 1; Mismatches 0;
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11-JUL-2000; 2000US-00614150.
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                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL30511), expressed DNA ABB12072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKAAKDLVLGPSGVLQGIRP--GKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNQ
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                                                                                                                                                                                                DB 4; Length
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                                                                                                                                                                                               26.8%; Score 769.5; DB 4 32.6%; Pred. No. 1.5e-61; iive 108; Mismatches 222
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                                      ID NO 9582;
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     Drosophila
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                                                                                                                                                                              Sequence 574 AA;
                                      Disclosure; SEQ
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The invention relates to nucleic acid fragments encoding branched chain amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutryate dehydrospenase, 3-hydroxymethylglutaryl CoA (HMG-COA) lyase and isovaleryl-CoA dehydrogenase polypeptides and polymucleotides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. Polymucleotides of the invention can be used as probes for physical mapping of genomes. The present sequence is corn 3-hydroxyisobutyrate dehydrogenase (BC 11.1.1.31) from crln.pk0191.blo, p0076.cwhan08r and
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produce transgenic plants having an altered expression of the enzyme.
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Branched chain amino acid degradation enzyme; HMG-CoA lyase;
3-bydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA;
isovaleryl-CoA dehydrogenase; transgenic plant; corn; EC 1.1.1.31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 733; DB 5;
Pred. No. 1.6e-58;
7; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                            JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Rafalski
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑJ,
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                                                                                                                                                                                                                                                                                                                                                                                         (DUPO ) DU PONT DE NEMOURS & CO
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52.3%;
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                                                                                                                                                                                                                                                                                 99US-00364230
                                                                                                                                                                                                                                                                                                                                       98US-0094990P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 52.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dehydrogenase (EC 1.1
p0118.chsbe01r clones
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hitz WD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD31748
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Alpha-methylene-gamma-butyrolactone; glutamate decarboxylase; herbicide; enzyme; gamma-aminobutyrate aminotransferase; UDP-glucosyltransferase; gamma-hydroxybutyrate dehydrogenase; tulipalin A; plant.
                                                                                                 DU PONT DE NEMOURS & CO
                                                                      .0-JUN-2002; 2002WO-US018230
                                                                                    08-JUN-2001; 2001US-0297198P
                                                                                                                    Flint D,
                                                                                                                                 2003-201331/19.
                                                                                                       (PRAB/) PRABHU V.
                                                                                                                                        N-PSDB; AAD55024
                                             WO2002101013-A2
                                Tulip pistil
                                                           19-DEC-2002
                                                                                                                    HG,
                                                                                                 (DADA)
                                                                                                                    Damude
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Prabhu V,

The invention relates to genes encoding key enzymes in the biosynthesis of alpha-methylone-gamma-butyrolactone (tulipalin A). Key enzymes include glutamate decarboxylase, gamma-aminobutyrate aminotransferase, gamma-hydroxybutyrate dehydrosyntransferase. The invention is useful for producing tulipalin A or tuliposide A or its pathway intermediates such as apha-methylenesuccinate semialdehyde, alphamethylene-gamma-aminobutyrate or alpha-methylene-gamma-hydroxybutyrate. Tulipalin A sequences are used to immunise animals to produce polyclonal randocinal antibodies with specificity for them or as targets to facilitate design and/or identification of inhibitors of those enzymes gamma-hydroxybutyrate dehydrogenase homologue Novel isolated nucleic acid fragment encoding a tuliposide A synthesizing protein, useful for creating recombinant organisms that have the ability to synthesize tulipalin A, tuliposide A or tuliposide A pathway intermediates. Claim 4; Page 110-111; 71pp; English. Sequence 290 AA;

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269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                                               388
                                                                                                                                                                                                                   448
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                                                                                                                                                              EVGFLGLGIMGKAMAVNLLRSGFRVTVWNRTLSKCNELLEGGASVGETPAAVIKKCKYTI
                                                                                                                                      ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                         GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
                                                                                                                                                                                                                                                                           449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQXDLR
                                                                                                                                                                                                                                         122 GSKKPAEDĠQLVILAAĞEKALYEEIIPAFEVLGKKSFFLGQVGNGANMKLIVNMIMGSMM
                                                                                                                                                                                                                                                                                                          182 NALSEGLSLAGKSGLEÇKTLLDVLDLGAIANPMFKLKGPAMIQNNHPPAFPLKHQQKDMR
                                           0; Gaps
   25.1%; Score 720; DB 6; Length 290; 50.7%; Pred. No. 1.8e-57; ive 52; Mismatches 86; Indels
                                       86; Indels
                                                                                                                                                                                                                                                                                                                                               LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548
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|Lalalgdenavsmpvaaaneafkkarslglgdldfsavy 281
Query Match
Best Local Similarity 50.77
Matches 142; Conservative
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AAE36392 standard; protein; 289 AA.

RESULT 20 AAE36392 ID AAE36

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The invention relates to genes encoding key enzymes in the biosynthesis of alpha-methylene-gamma-butyrolactone (tulipalin A). Key enzymes include glutamate decarboxylase, gamma-aminobutyrate aminotransferase, gamma-hydroxybutyrate dehydrogenase and UDP-glucosyltransferase. The invention is useful for producing tulipalin A or tuliposide A or its pathway intermediates such as alpha-methylenesuccinate semialdehyde, alpha-methylene-gamma-hydroxybutyrate. Tulipalin A sequences are used to immunise animals to produce polyclonal ranibodies with specificity for them or as targets to a monoclonal antibodies with specificity for them or as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. The present sequence is mouse-ear cress (Arabidopsis thaliana) gamma-hydroxybutyrate dehydrogenase homologue
                                                                                                                                                                                                   Alpha-methylene-gamma-butyrolactone; glutamate decarboxylase; herbicide;
enzyme; gamma-aminobutyrate aminotransferase; UDP-glucosyltransferase;
gamma-hydroxybutyrate dehydrogenase; tulipalin A; plant; mouse-ear cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid fragment encoding a tuliposide A synthesizing protein, useful for creating recombinant organisms that have the ability to synthesize tulipalin A, tuliposide A or tuliposide A pathway
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    A. thaliana gamma-hydroxybutyrate dehydrogenase homologue.

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; Pred. No. 3.7e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; Page 112-113; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE NEMOURS & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUN-2002; 2002WO-US018230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-2001; 2001US-0297198P.
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                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-201331/19.
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PRABHU V.
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                                                                                                                                                                                                                                                                                                                                                                                       WO2002101013-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intermediates.
                                                                                         26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9-DEC-2002
                               AAE36392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGR 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polymucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used to produce transgenic plants having an altered expression of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutyrate dehydrogenase, 3-hydroxymethylglutaryl CoA (HMG-CoA) lyase and isovaleryl-CoA dehydrogenase polypeptides and polymuclectides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. Polymucleotides of the invention can be used as probes for physical mapping of genomes. The present sequence is soybean 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) from ses2w.pk0002.e5 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to nucleic acid fragments encoding branched chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Branched chain amino acid degradation enzyme; HMG-CoA lyase;
3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA;
isovaleryl-CoA dehydrogenase; transgenic plant; soybean; BC 1.1.1.31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.8%; Score 682; DB 5; Length 345; 47.1%; Pred. No. 7.7e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
242 LALALGDENAVSMPVAAAANEAFKKARSLGLGDLDFSAVIEA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99;
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                                                                                                                                                                                                                                                    Soybean 3-hydroxyisobutyrate dehydrogenase #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rafalski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                      AAE19929 standard; protein; 345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Col 33-36; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinney AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0094990P.
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Matches 136; Conservative
                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cahoon RE, Hitz WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-204621/26.
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N-PSDB; AAD31750
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                                                                                                                                                                                                                                                                                                                                                                                                                                             US6348339-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166
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Best Local S
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                                                                                                                                                                     AAE19929;
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AAC AAE1

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The present sequence represents a plant gamma-hydroxy butyrate dehydrogenase (GHBDH). The specification also describes a plant gamma-minobutyric acid (GABA) transaminase (GABA-T). The proteins are involved in the metabolism of GABA in plants. GABA-T is used to transaminate GABA to form succinic semialdehyde, which may be converted to gamma hydroxybutyrate by GHBDH. The polynucleotides are used to produce GABA-T and GHBDH recombinantly. The proteins are useful for screening and isolation of homologous genes from other organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel proteins related to gamma aminobutyric acid (GABA) metabolism, GABA-transaminase and gamma hydroxy butyrate dehydrogenase useful for screening and isolation of homologous genes from other organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 1. .100 /note= "these residues are encoded by nucleotides 1-300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 AMLSDPCAALSVVFDKGGVLEQICEGKGYIDMSTVDABTSLKINEAITGKGGRFVEGPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVGFIGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVEHGASVCESPAEVIKKCKYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gamma-aminobutyric acid; GABA; GABA transaminase; GABA-T;
gamma-hydroxy butyrate dehydrogenase; GHBDH; succinic semialdehyde;
                                                                                                                                                                                                                                                                                                             Amino acid sequence of gamma-hydroxy butyrate dehydrogenase (GHBDH)
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286 HQQKDLRLALGLAESVSQPTPIASAANELYKVAKSNGLSDQDFSAVIEA 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Cauwenberghe OR;
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                                                                                                                                                     AAB19491 standard; protein; 289
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Best Local Similarity 48.65
Matches 137; Conservative
                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                     gamma-hydroxy butyrate
gamma hydroxybutyrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
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990S-013978-090S-0140832P.
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                                  18 - JUN - 1999;
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29-JUN-1999;
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01-JUL-1999;
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23-JUN-1999;
24-JUN-1999;
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16-JUL-1999;
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23-JUL-1999;
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03-AUG-1999
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04-AUG-1999;
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          182 NAFSEGLVLADKSGLSSDTLXXIXDLGAMTNPMFKGKGPSMTKSSYPPAFPLKHQQKDMR 241
                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                          Arabidopsis thaliana protein fragment SEQ ID NO: 8739.
                           509 LAIALGDAVNHPTPMAAAANEVYKRAKALDOSDNDMSAVYRA
                                                                                                                     AAG10423 standard; protein; 353 AA
                                                                                                                                                                                                                                                                                                                                                                                   990S-0121825P.
990S-0125188P.
990S-0125788P.
990S-0126784P.
990S-0127462P.
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990S-013144P.
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990S-0132486P.
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                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                              Arabidopsis thaliana
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06-APR-1999;
08-APR-1999;
16-APR-1999;
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30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
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14-JUN-1999;
16-JUN-1999;
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23-APR-1999;
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21-MAY-1999;
24-MAY-1999;
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29-MAR-1999
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14-MAY-1999;
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19-MAY-1999
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14-MAY-19
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28-APR-1
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418 QAMGKISFFLGEVGNAAKMMLIVNNVQGSFWATIAEGLTLAHVTGQSQQTLLDILNQGQL 477
                                                                                                                         478 ASIFLDQKCQNILQGNFKPDFYLKYIQKDLRLALALGDAVNHPTPMAAAANEVYKRAKAL 537
                                                                                                                                  272 NAPMYSLKGPSMIKSVYPTAFPLKHQQKDMRLALGLAESVSQSTPIAAAANBLYKVAKSY 331
                                                         358 VDMSTVDADIVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCF 417
                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
RTAEKCDLF1QEGARLGRTPAEVVSTCD1TFACVSDPKAAKDLVLGPSGVLQG1RPGKCY
                                   Arabidopsis thaliana protein fragment SEQ ID NO: 8740.
                                                                                                                                                                                                                    AAG10424 standard; protein; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   990S-0126264P.
990S-0126785P.
990S-0127462P.
990S-0128714P.
990S-0128714P.
990S-0138714P.
990S-0130449P.
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990S-0131449P.
990S-0131449P.
990S-0132484P.
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990S-0132486P.
990S-0132487P.
990S-0132863P.
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99US-0123180P.
99US-0123548P.
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                                                                                                                                                           538 DOSDNDMSAVYRA 550
                                                                                                                                                                            332 GLŚDEDFSAVIEA 344
                                                                                                                                                                                                                                                      (first entry)
            51 TTPSTRDELGTVS-
                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
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05-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2000;
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25-MAR-1999;
29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000
                                                                                                                                                                                                                                      AAG10424;
                             298
                                             92
                                                                              152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.3%; Score 667.5; DB 3; 39.1%; Pred, No. 1.7e-52; ive 65; Mismatches 121;
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99US-0158332P.
99US-0158369P.
99US-0159294P.
99US-0159295P.
99US-0159239P.
99US-0159339P.
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990S-0159638P
990S-0160584P
990S-0160767P
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990S-0160814P
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990S-0160981P
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990S-0161360P.
990S-0161361P.
990S-0161920P.
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990S-0152363P.
990S-0153070P.
990S-015378P.
990S-0154039P.
                               9905-0149175E
9905-0149426E
9905-0149722P
9905-0149929P
9905-0149929P
9905-0149930P
9905-015086E
9905-015086E
9905-015086E
9905-015066F
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99US-0157117P.
99US-0157753P.
99US-0157865P.
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99US-0155486P.
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99US-0156458P.
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99US-0148684P.
99US-0149368P.
                                                                                                                                 99US-0151303P
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Best Local Similarity 39.1%
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1999;
29-OCT-1999;
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14-0CT-1999;
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18-AUG-1999;
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23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
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27-AUG-1999;
30-AUG-1999;
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                                                                                                  -AUG-1999;
-AUG-1999;
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14-0CT-1999
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99US-0134218P. 99US-0134219P. 99US-0134221P. 99US-0134370P.

14-MAY-1999; 14-MAY-1999; 14-MAY-1999;

SSTVKGM----MAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVC----YQAITK 237

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238 KLKICEBETGSTSIQAADSTAVNGSITFTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWN 297 SSSSKAMALCSICPRIPLRFRPKPISP-----PL---SKPQICLAYRVYSSLQS

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02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
06-AUG-1999;
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99US-0143542P.
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19-JUL-1999;
19-JUL-1999;
       30-APR-1999;
30-APR-1999;
04-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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11-MAY-1999;
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14-MAY-1999
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 GNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNIL 490
                                                                                                                                                                                                                                                                                          550
                                                                                                                                             251 IQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEG 310
                                                                                                                                                                                ARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTE 370
                                                                                                                                                                                                                    LAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEV 430
                                                                                                                                                                                                                                                                   215 GNGAAMKLVVMMIMGSMMASFAEGILLSQKVGLDPNVLVEVVSQGAINAPMYSLKGPSMI 274
                                                                                                           196 PMAAFKWOPTASEPVKDADPHFHHFLLSQTEKPAVC----YQAITKKLKICEBETGSTS 250
                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                      QGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA
                                                                                                                                                                                                                                                                                                   116; Indels 38; Gaps
                                                                       23.3%; Score 667; DB 3; Length 343; 39.4%; Pred. No. 1.9e-52; ive 64; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 8741.
                                                                                                                                                                                                                                                                                                                                                          AAG10425 standard; protein; 285 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0121825P.
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99US-0161932P.
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                                                                                   Best_Local Similarity 39.4
Matches 142; Conservative
                                                                                                                         | ::| |
PRIPLRFRPKPISP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
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06-APR-1999;
08-APR-1999;
16-APR-1999;
19-APR-1999;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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23-APR-1999;
23-APR-1999;
   26-OCT-1999;
26-OCT-1999;
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28-OCT-1999;
28-OCT-1999;
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                                                                           Query Match
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99US-014930B

99US-015103B

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14-0CT-1999;
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02-AUG-1999
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14-OCT-1999;
14-OCT-1999;
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26-AUG-1999
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27-AUG-1999
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15-SEP-1999;
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03-AUG-19
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                                                                                                                                                                                                                                                                                                                                          61 ESAIDVACGKNGAIFGISSGKGYVDVSTVDVASSILISKQIKDTGALFLEAPVSGSKKPA 120
                                                                                                                                                                                                                                                                                                                                                                            454
                                                                                                                                                                                                                                                                                                                                                                                                                                   395 NDGMLVILAAGDRGLYEDCSSCRQAMGKTSFRLGEVGNAAKMMLLVNMVQGSFMATIAEG
                                                                                                                                                                                                                                                                                                                                                                                     455 LTLAHVTGQSQQTLLDIINQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALG
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Branched chain amino acid degradation enzyme; HMG-COA lyase; 3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl COA; isovaleryl-CoA dehydrogenase; transgenic plant; corn; EC 1.1.131.
                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                   Query Match
21.9%; Score 629; DB 3; Length 285;
Best Local Similarity 45.3%; Pred. No. 4.4e-49;
Matches 125; Conservative 56; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               515 DAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corn 3-hydroxyisobutyrate dehydrogenase #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Unknown
/note= "Encoded by NTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Unknown
/note= "Encoded by NCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE19926 standard; protein; 247 AA
99US-0160741P-
99US-0160741P-
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99US-016070P-
99US-01608114P-
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99US-016136P-
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29-JUN-1999;
30-JUN-1999;
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                                                 25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
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28-APR-1999;
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The invention relates to nucleic acid fragments encoding branched chain amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutyrate dehydrogenase, 3-hydroxymethylglutaryl CoA (HWG-CoA) lyase and isovaleryl-CoA dehydrogenase polypeptides and polynucleotides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. Polynucleotides of the invention can be used as probes for physical mapping of genomes. The present sequence is corn 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) from cen3n.pk0138.e1, cta1n.pk0052.d10 and p0037.crwak74r clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 SNLLKWGHTVTVWNRTABKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNNVQGSFMATIAEGLTLAHVTGQ 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used to produce transgenic plants having an altered expression of the enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 SNLIKAGCDVTVWNRTKSKCDPLLSLGAKYEPTPAQVASSCDVTFAMLADPQSAAEVACG
                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 SQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAV 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPNTLVEVISQGAISAPMFSLKGPSMVKAAYPPAFPLKHQQKDLS-SIGLADRV 234
                                                                                                                                                                                                                                                                                                                                                                                             18.8%; Score 537.5; DB 5; Length 247; 45.3%; Pred. No. 9.8e-41; ive 47; Mismatches 80; Indels 1;
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                                                                                               Kinney AJ, Rafalski JA;
                                                                                                                                                                                                      Disclosure; Col 23-26; 40pp; English.
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                     99US-00364230.
                                              98US-0094990P
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106; Conservative
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                                                                                                                         WPI; 2002-204621/26
                                                                                                                                                                                                                                                                                                                                                                           Sequence 247 AA;
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                     29-JUL-1999;
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01-SEP-1999;
07-SEP-1999;
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29-SEP-1999;
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269 KIGFLGLGLMGSGIVSNILKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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99US-015753P

99US-0158029P

99US-0158029P

99US-0159294P

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05-0CT-1999;
06-0CT-1999;
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RESULT 30 AAG20954 ID AAG20954 standard; protein; 336 AA.

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Db	26	26 ASSTISSDIITPSNTKIGWIGTGVMGRSMCGHLIKAGYTVTVFNRTISKAQTLIDMGANV 85	IGWIGTG	VMGRSMCC	SHLIKAGYT	VTVFNRTI	SKAQTLİ	DMGANV	85	
ζζ	314	314 GRIPAEVVSTCDITFACVSDPKAAKDLVLGP-SGVLQGIRPGKCYVDMSTVDADIVTELA 372	CVSDPKA	AKDLVLGI	TCDITFACVSDPKAAKDLVLGP-SGVLQGIRPGKCYVDMSTVDADTVTELA	RPGKCYVD	MSTVDAD	TVTELA	372	
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οy	373	373 QVIVSRGGRFLEAPVSGNQQLSNDGMLV1LAAGDRGLYEDCSSCFQAMGKTSFFLGEVGN 432	GNQQLSN	IDGMLVIL!	AAGDRGLYE	YEDCSSCFQAMGKTSFFLGE	MGKTSFF	LGEVGN	432	
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δλ	433	433 AAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQG 492	ATIAEGI	TLAHVTG	SQQTLLDI	LNOGOLAS	IFLDOKO	ZONILOG	492	
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Search completed: September 16, 2004, 07:30:35 Job time : 69 secs

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OM protein - protein search, using sw model

Run on:

September 16, 2004, 07:28:53; Search time 19 Seconds (without alignments) 1502.587 Million cell updates/sec

Title: Perfect score:

US-10-067-482-2 2866 1 MAAVSLRLGDLVWGKLGRYP.....AKALDQSDNDMSAVYRAYIH 553

Scoring table: Sequence:

389414 seqs, 51625971 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Database

lsgued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description	Seguence	Seguence	Segmence	Sequence	Segmence	Sequence	Sequence	Segmence	Seguence	Segmence	Segmence	Semience	Segmence	Semience	Sequence	Sementes	Seguence	Seguence	Seguence	Sequence	Seguence	Seguence	Semience	Segmence	Sementer	Segmence	Sequence
SUMMARIES	ţ	U.L.	US-10-164-595-72	US-09-364-230-4	US-09-364-230-8	-364-	9	US-09-328-352-7407	9	US-09-107-532A-5109	US-09-489-039A-9424	US-09-252-991A-26001	-252-	9-711-	US-09-252-991A-24727	9-328-352-487	9-328-352-813	364-230-6	6	US-09-364-230-12	US-09-489-039A-9860	US-09-489-039A-11448	9	US-08-760-745-5	US-08-760-745-3	-760-745-	-09	US-09-788-657-22	39
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	0	arone	2811	733	682	537.5	364	343.5	343	340	326	324.5	310	301.5	291	287.5	266	258.5	252	240.5	226.5	224.5	208	185.5	185.5	178.5	161.5	148.5	145
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                                                                                                                                                                                                                                                              Gaps
                                              APPLICANT: Origene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 10 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
ERNGTH: 547
                                                                                                                                                                                                                                                              . 9
                                                                                                                                                                                                                               Score 2811; DB 4; Length 547;
Pred. No. 3.6e-261;
0; Mismatches 1; Indels
        ; Sequence 72, Application US/10164595; Patent No. 6657054; GENERAL INFORMATION:
                                                                                                                                                                                                                                     98.1%;
98.7%;
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                                                                                                                                                                                                                                                                 Matches 546; Conservative
                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                 Similarity
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US-10-164-595-72
JS-10-164-595-72
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Sequence 4, Application US/09364230 Patent No. 6348339 GENERAL INFORMATION:

RESULT 2 US-09-364-230-4

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APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Arthony J.
APPLICANT: Rafalski, J. Anthony.
APPLICANT: Rafalski, J. Anthoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: BB-1178
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT FILING DATE: 1999-07-29
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cahoon, Rebecca E.
APPLICANT: Kinney, Althony J.
APPLICANT: Kinney, Althony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, J. Ah coni
TITLE OF INVENTION: Blaymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: BB-1178
CURRENT PELLING DATE: 1999-07-29
BARLIER APPLICATION NUMBER: 60/094,990
BARLIER APPLICATION NUMBER: 60/094,990
BARLIER PILING DATE: July 31, 1998
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 446 SFMATIAEGLILAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQK 505
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23.8%; Score 682; DB 4; Length 345;
Best Local Similarity 47.1%; Pred. No. 5.7e-57;
Matches 136; Conservative 54; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Length 360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.6%; Score 733; DB 4; 52.3%; Pred. No. 7.7e-62; tive 47; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application US/09364230; Parent No. 6348339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Glycine max
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Best Local Similarity
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US-09-364-230-8
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GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PEPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US/6/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 KIGFLGLGLMGSGIVSNILKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
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Patent No. 6562958
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ORGANISM: Klebsiella pneumoniae
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Best Local Similarity
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Matches 79; Conserv
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US-09-328-352-7407
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hitz, Milliam D.
APPLICANT: Hitz, Milliam D.
APPLICANT: Kainsky, Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: BB-1178
CURRENT APPLICATION NUMBER: US/99/364,230
CURRENT APPLICATION DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER FILING DATE: July 31, 1998
                                             STCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTBLAQVIVSRGGR 381
                                                                                                                                382 FLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVN 441
                                                                                                                                                                                       FLEAPVSGSKKPAEDGQLIFLTAGDKNLYEAVGSLLDIMGKSKFYLGDVGNGAAMKLVVN 225
                                                                                                                                                                                                                                                       MVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLK 501
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45.3%; Pred. No. 2.5e-43;
live 47; Mismatches 8(
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Matches 106; Conservative
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ORGANISM: Zea mays
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NAME/KEY: UNSURE
LOCATION: (244)
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389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448 

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Sequence 9294, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:

US-09-489-039A-9294

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GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKPDFYLKYIQKDLRLALALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVYRAYIH 553
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                                                   | | | : | | | | | | : | | | | | | EDPGFRISHQONFSTCAAIGGSNWDHSALIKGLEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SPLKRAQEQSPRKRGRPP----KDEKULTIPESSTVKGMMAGPMAAFKWQPTAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 -PLRAPGPHRLPGLDRLRVQAGHHH-----RSRPRLDEDAQRRLIRTHEQDAPASLRGAT
                      449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.0%; Score 343; DB 4; Length 543; 23.5%; Pred. No. 4.4e-24; ive 83; Mismatches 212; Indels
                                                                                                                            509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 GPHPGKPVGGDÓPRATRROPRPPRTGHRRDOLPL--
                                                                                                                                                                                                                              Sequence 27650, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MATC J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OKGANISM: FSEULO
US-09-252-991A-27650
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US-09-107-532A-5109
                                                                                                                                                                                                   RESULT 7
US-09-252-991A-27650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simil
Matches 113; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 543
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
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                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 340; DB 4; 1
Pred. No. 3.2e-24;
2; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
;
; LOCATION: (B) LOCATION 1...299
; SEQUENCE DESCRIPTION: SEQ ID NO: 5109:
US-09-107-532A-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEBHONR: (781) 893-8077
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 5109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
PAPPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            509 LAIALGDAVNHPTPMAAAANEVYK 532
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                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: <Unknown>
                                                                                                                                                STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 299 amino acids
TYPE: amino acid
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                                                                                                                                                                                               STATE: Massachusetts
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28.8%;
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Best Local Similarity 28.8<sup>§</sup>
Matches 76; Conservative
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                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                          CITY: Waltham
                                                                                                                                                                                                                       COUNTRY: USA
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RESULT

Sequence 5109, Application US/09107532A Patent No. 6583275

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Sequence 17923, Application US/09252991A
Patent No. 6521795
Releand INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PILLING DATE: 1999-02-18
REIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17923
                                                                                                                                                                                                                                                                220 QGLABALHFARCAGLDGBAAMQVIGKGAAQSWQLENRHQSMLAGEFDFGFAVDWMRKDLS 279
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                                         329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 LAFAGLGLMGVPMCRRLLAAGYPLAVWNRSPGKRELLAAEGAKAVEVPABLAADAEILML 101
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                                                                                                                                389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
                                                                     100 CCVGNDDDLRAVALGEQGAFAGMAPGSLFVDHTTASAEVARELSLLAAERELGFLDAPVS
                                                                                                                                                                449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 330;
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Patent No. 6589738
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
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Ohlsen, Kari
Zyskind, Judith
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Batent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26001
LENGTH: 324
                                                                     GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 VSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 VSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.4%; Score 326; DB 4; Length 304;
29.9%; Pred. No. 7.4e-23;
Live 52; Mismatches 136; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGA-RLGRTPAEVVSTCDITF
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                                                                                                                                                             FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9424
US-09-489-039A-9424
; Sequence 9424, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Klebsiella pneumoniae
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les 74; Conservative
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Matches
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Matches
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APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4879, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
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PVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIV-NMVQ 444
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US-09-328-352-8139
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Best Local Similarity
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US-09-328-352-8139
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US-09-328-352-4879
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                GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24727
LENGTH: 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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; Pred. No. 1.6e-20;
51; Mismatches 152;
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1 Similarity 28.9%; Pred. No. 1.6e-19;
82; Conservative 57; Mismatches 135
                          TITLE OF INVENTION: GENES ESSENTIAL FOR MI FILE REFERENCE: ELITRA.008A CURRENT APPLICATION NUMBER: US/09/711,164 CURRENT FILLING DATE: 2000-11-09 PRIOR APPLICATION NUMBER: US 60/164415 PRIOR FILING DATE: 1999-11-9 NUMBER OF SEQ ID NOS: 469 SOFTWARE: FASTSEQ FOR Windows Version 4.0
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27.7%;
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ORGANISM: Escherichia coli
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Best Local Similarity
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LENGTH: 292
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US-09-364-230-12
Sequence 12, Application US/09364230
SAPPLICANT: Cahoon, Rebecca E.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, Milliam D.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: BB-1178
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT FILING DATE: 1999-07-29
EARLIER PILING DATE: J099-07-29
SERRIER FILING DATE: J099-07-29
SOFTWARE: Microsoft Office 97
                                                                                                                                                               Sequence 5460, Application US/09134000C
Patent No. 6617156
GENERAL INPORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
FRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 MMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFK 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AEVGAHALDAEVSGGDLGAKNGTLTIMVGGDQESYDTVLPIFKTFGKTFMLHGSAGKGQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

8.8%; Score 252; DB 4; Length 24
Best Local Similarity 26.7%; Pred. No. 6.7e-16;
Matches 58; Conservative 41; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 PDFYLKYIQKDLRLAIALGDAVNHPTPMAAANEVYK 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 IYRKLCADGCELKDFSCAFR 333
530 VYKRAKALDQSDNDMSAVYR 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Triticum aestivum
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LOCATION: (154)
FEATURE:
NAME/KEY: UNSURE
                                                                                                                                           US-09-134-000C-5460
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LENGTH: 350
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APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
CURRENT APPLICATION NUMBER: US/09/364,230
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 6
LENGTH: 342
                                                                                                270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGA------RLGRTPAEVVST 323
                                                                                                                                                  IAFLGIGLMGSRMASRLIQAGFQVAVWNRTTSACEELIDIGAHALDLSNIGQYP----- 100
                                                                                                                                                                                                324 CDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFL 383
                                                                                                                                                                                                                                 384 EAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMV 443
                                                                                                                                                                                                                                                                                                                            216 VAANSALIAEAVALADRAGVDTTLLAPALAGG-----FADSKPPQILAPRNATHTFEFVQ 270
                                                                                                                                                                                                                                                                                                                                                                                              444 QGSFWATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNIL-----QGNFKP-D 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 TPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPCKC----YVDMSTVDADTVTE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 SPLEVSKSSDVVITMLPSSAHVLDVYNGRNGLLAN---GGCLGPWLYIDSPTVDPQTSRK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 LAQVI------VSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Gaps
                                                            28;
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                 Length 326;
     9.3%; Score 266; DB 4; Length 32.
28.9%; Pred. No. 4.8e-17;
ative 42; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYLKYIQKDLRLAIALGDAVNHPTPMAAAA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09364230 Patent No. 6348339 GENERAL INFORMATION:
Query Match
Best Local Similarity 28.9%
Matches 78, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 81; Conserv
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: GATY Breton et. al

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999.01.29

PRIOR FILING DATE: 1999.01.29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 IQEGARLGRIPABV--VSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 ADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTS 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 NRMQHVLDGDYSPKSAVDIFVKDLGLVNDTARALTFPLPLPLATTALNMFTSASNAGFGRED 291
172 YRIGSDIGLGSTVKIIHQLLAGVHIAVAAEAMALAARAGIPLETMYDVVTHAAGUSWMFF 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425 FFLG-EVGNAARAMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDIINOGQLASIFLD
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                                              484 QKCQNILQGNEKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANBVYKRAKALDQSDND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.8%; Score 224.5; DB 4; 22.4%; Pred. No. 4.3e-13; tive 63; Mismatches 161;
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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; Sequence 22003, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                          US-09-489-039A-11448
; Sequence 11448, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 14342
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Best Local Similarity
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Sequence 9860, Application US/09489039A
Sequence 9860, Application US/09489039A
Betent No. 6510836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                                                                                                       378 RGGR-----FLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGN 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 TGVPSSRNYDGGFTSKLMAKDLDLAMASASGVGFKCPMGSEALEIYRKLCDEGCEFKDFS 337
                                                                                                                                                                                                                                                    265 PIDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTC 324
                                                                                                                                                                                                                                                                                                                                           DITFACVSDPKAAKDLVLGPSGVL-QGIRPGK-CYVDMSTVDADTVTELAQ-----VIVS 377
                                                                                                                                                                                                                                                                                                                                                                                  DVVITMLPSSAHVLDVYSGRNGLLGNGGRLGPWLYIDSSTVDPHTSRKISMDMSRCXLNE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
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                                                                                                                                                             Length 350;
                                                                                                                                                                                                         Indels
                                                                                                                                                           8.4%; Score 240.5; DB 4;
26.1%; Pred. No. 1.5e-14;
tive 41; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                Conservative
                                                                                    ; LOCATION: (184)...(201)
US-09-364-230-12
                                                                                                                                                             Query Match
Best Local Similarity
Matches 80; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-489-039A-9860
                                                                           NAME/KEY: UNSURE
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US-09-489-039A-9860
                             LOCATION: (176)
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                                                       FEATURE:
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67 KEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSGDEK 126
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                                                                                                                                                                                                                                                                                                                                                    127 RKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKR----AQEQSPRKRGRPFK----D 177
                                                                                                                                                                                                                                11 KCGDLVFAKMKGYPHWPARIDEMPEAAVKSTANK-YQVFFFGTHETAFLGPKDLFPYEES 69
                                                                                                                                                                                        7 RIGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHAH 66
                                                                                                                                                       27;
                                                                                                                    Length 237;
                                                                                                                                                       94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 178 EKDLTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.5%; Score 185.5; DB 2;
Best Local Similarity 29.8%; Pred. No. 1.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Murry, Lynn B.
TITLE OF INVENTION: LUNG GROWTH FACTOR VARIANT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                   32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0169 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/760,745
FILING DATE: Herewith
CLESSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08760745
Patent No. 5972658
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                   65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
              IMMEDIATE SOURCE:
                               LIBRARY: GenBa
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US-08-760-745-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY:
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                                                                                                                                                                                                                                                                                                                                       330 CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSG 389
                                                                                                                                                                                                                                                                                                                                                                           69 MLPAGGHVESLYLGDDGLLARVAGKPLLIDCSTIAPETARKVAEAAAAKGLTLLDAPVSG 128
                                                                                                                                                                                                                                                                                                                                                                                                                    390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 GVGGARAĞTLSFIVGGPAEGFARARPVLENMGRNIFHAGDHGAGQVAKICNNMLLGILMA 188
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                              7.3%; Score 208; DB 4; Length 221; 27.5%; Pred. No. 9.5e-12; vative 36; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08760745
; Sequence 5, Application US/08760745
; Patent No. 5972658
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Marry, Lynn E.
; TITLE OF INVENTION: LUNG GROWTH FACTOR VARIANT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
CONTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FASTERY DOS
SOFTWARE: FASTERO VERSION 2.0
CURRENT APPLICATION DATA:
RILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
RELING DATE:
FILING DATE:
ATTORNET:
PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FLILMG DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 22003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET WIMBER: PF-0169 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                 TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                        Query Match 7.3%
Best Local Similarity 27.5%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   450 TIAEGLTLAHVTG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 GTAEALALGVKNG 201
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linear
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Sequence 10, Application US/09364230

Sequence 10, Application US/09364230

Sequence 10, Application US/09364230

Sequence 10, Application US/09364230

Sequence 10, Application US/09364230

APPLICANT: Rafalaki. J. Antoni

TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids

FILE REFRENCE: Bell 178

CURRENT APPLICATION NUMBER: US/09/364,230

CURRENT APPLICATION NUMBER: 60/094,990

EARLIER FILING DATE: 1999-07-29

EARLIER FILING DATE: July 31, 1998

NUMBER OF SEQ ID NOS: 34

SOSTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 VDMSTVDADTVTELAQVIVS-----RGGRF-----LEAPVSGNQQLSNDGMLVILAAGDR 407
                                                                               69 EMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSGDEKRK 128
                                                                                                                                                                      129 LSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQ----EQSPR--KRGRPPKDEKDLT 182
                                                                                                                                                                                                             122 -GNAEGSSDE----EGKLVIDEPAKEKNEKGALKRRAGDILEDSPKRPKEAENPEGEE--- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408 GLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 EAFLAAKPILFSMGKSAIXCGGAGSGSAAKICNNLALAVSMLGISEALALGQSLGVSAST 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 LLDILNQGQLASIFLD--QXCQNILQ-----GNFKPDFYLKYIQKDLRLAIALGDAVNHP 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 LTNIFNCSSARCWSSDAYNPVPGLMEGVPSSGDYNGGFASKLMAKDLNLAVESAKLAGCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 LDSSTIDPQTSRNLSATVINYILREKKGDWEKPFKLDAPVSGSVJAAEAGTLTFMVGGSE
                         67 KFGKRNKRKGFSBGLWEIEN----NPTVKASGYQSSQKKSCVEEPEPEPEAAEGDGDKK
GDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTBDHAWIKVBQLKPYHAHKE
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APPLICANT: Sass, Philip
APPLICANT: Kinzler, Kenneth
APPLICANT: Grasso, Luis
APPLICANT: Grasso, Luis
APPLICANT: Ugelstein, Bert
TITLE OF INVENTION: Methods for generating hypermutable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.6%; Score 161.5; DB 4;
23.2%; Pred. No. 3e-07;
Live 36; Mismatches 109;
                                                                                                                                                                                                                                                               183 IPESSTVKGMMAGPMAAFKWQPTASEPVKDADP 215
                                                                                                                                                                                                                                                                                               194 YPLTSQAQKIYTELCSVGHEAKDFSCAFRHY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       521 TPMAAAANEVYKRAKALDQSDNDMSAVYRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/09788657; Patent No. 6656736; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Glycine max
US-09-364-230-10
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Best Local Similarity
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US-09-788-657-22
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                                                                                                                                                                                                                                                                                                    70 KEKFGKPNKRKGFSEGLWEIEN-----NPTVKASGYOSSOKKSCVEEPEPEPEAAEGDGD 124
                                                                                             7 RLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHAH 66
                                                                                                                                        69
                                                                                                                                    11 KCGDLVFAKMKGYPHWPARIDEMPEAAVKSTANK-YQVFFFGTHETAFLGPKDLFPYEES
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      Length 240;
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         ; Score 185.5; DB 2; Length; Pred. No. 1.6e-09; 30; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%; Score 178.5; DB 2;
29.6%; Pred. No. 7.1e-09;
tive 30; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                        180 ---KEAATLEVERPLPMEVEK-NSTPSEPGSGRGP 210
                                                                                                                                                                                                                                                                                                                                                               181 LIIPESSTVKGMMAGPMAAFKWQPTASEPVKDADP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LUNG GROWTH FACTOR VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08760745
Patent No. 5972658
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: LUNG GROWTH FACTOR VARIF
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0169 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTSEQ DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,745
FILING DATE: Herewith
CLASSIPICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
             6.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63; Conservative
                                                         64; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TOPOLOGY: linear
IMMEDIATE SOURCE:
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Best Local Similarity
Matches 63; Conserv
             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Pa.
STATE: CA
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US-08-760-745-1
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us-10-067-482-2.rai

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TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITIES OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR PRILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
            NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 QDTIRRNRELSAEGFNFIGTGVSGGEEGALKGPSIMPGGOKEAYELVAPILKQIAAVAED 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 CSSCFQAMGKISFFLGEVGNAAKMMLIVNMVQGSFWATIAE-----GLTLAHVTGQSQ 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 QTFTE-WNEGELSSYLID----ITKDIFTKKDEDVKYL----VDVILDEAANKGTGKW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 CDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LETPRRILLMVKAGAĞTDSAİDSLKPYLDK------GDIİIDGĞNTFF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 QQIGVVGMAVMGRNLALNIESRGYTVSVFNRSREKTEEVIAENPGKKLVPYYTVQEFVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQE--GARL--GRTPAEVVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTLLDILNQGQLASIFLDQKCQNILQGNF-KPDFYLKYIQKDLRLAIALGDAVNHPT---
                                                                                                                                                                                                                                                                                                                                                                                       94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                          Length 490;
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     4.8%; Score 139; DB 4; Length 486
l Similarity 19.2%; Pred. No. 0.00015;
64; Conservative 62; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                   54; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                       5.1%; Score 145; DB 4; 22.0%; Pred. No. 3.9e-05;
TITLE OF INVENTION: NUCLEAR FOR DIAGNOSTIC FLLE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER FO SEQ ID NOS: 14342
SEQ ID NO 8350
LENGTH: 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 EAPVSGNQOLSNDGMLVI---LAAGDRG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5380, Application US/095436B1A; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 TSQSSLDLGEPLSLITESVFAR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- PMAAAANEVYKR 533
                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                     71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: GARY BRETON
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||| |: || || : || || : :|| || 3 GDLVWAKWEGYPWPCLVYNNPFDGTFIREKGKSVRVHVQFFDDSPTRGWVSKRLLKPYT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 - EEKRRDEHRRRPDHPDFDASTLYVPEDFLNSCTPGMRKWWQIKSQNFDLVICYKVGKFY 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGR----T 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---DITFACV-SDPK-----AAKDLVLG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---APV-- 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 MMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKC---QNIL-Q 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       595 LFEKGN--LSKETKTILKSSLSCSLQEGLIPGSQFWDASKTLRTLLEEEFFREKLSDGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  553 VML-PQVLKGMTSESDSIGLT----PGEKSELALSALG----GCVFYLKKCLIDQELLSM
                                                                                                                                                                                                                                                                                                                                                                                                                         9 GDLVWGKLGRYPPWPGKIVNPPKD--LKKPRGKKC-FFVKFF-GTEDHAMIKVEQLKPYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 GSKSK--EAQKGGHFYSAKPEILRAMORADEALNKDKIKRLELAVCDEPSEPEBEBEBENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 GTTYVTDKSEEDNEIESEEEVQPKTQGSRRSSRQIKKRRVISDSESDIGGSDVEFKPDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 GMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQ------TEKPAVCYQAITKKLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TSSHNSSDDKNRRNSSEERSRPNSGD-----EKRKLSLSEGKVKKNMGEGK----
                                                                                                                                                                                                                                                                                                                                                                                   239;
                                                                                                                                                                                                                                                                                                                                  DB 4; Length 1360;
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    704 ANFE----EYIPLD-----SDTVS-TTRSGAIFTKAYQR 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 GNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKR 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 PSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLE--
                                                                                                                                                                                                                                                                                                                                                                                89; Mismatches 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 AHKEEMIKINKGKRFQQAVDAVEEFLRRAK---GKDQ-
                                                                                                                                                                                                                                                                                                                                  5.2%; Score 148.5; DB 19.9%; Pred. No. 9.7e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 CEEETGSTSIQAADSTAVN------GSITP--
  FILE OF INVENTION: yeast
CURRENT APPLICATION NUMBER: US/09/788,657
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/184,336
PRIOR PILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 SETKNTLRAFS-APONSE-
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 PAEVVSTC-----
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
hes 140; Conserv
                                                                                                                                                                                                                    1360
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320 VVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRG 379

260 NGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAE 14 DGSYFMSKQOIGVVGMAVMGRNLALNIESRGYTVSIYNRSSDKTNEVIAENPGKKLVPNY

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Sequence 8350, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:

US-09-489-039A-8350

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APPLICANT: Gary Breton et.

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PatentIn version 3.0
 2000-06-02
              NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin v
SEQ ID NO 2
LENGTH: 786
TYPE: PRT
CURRENT FILING DATE:
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                                                                                           sb.
                                                                                        , ORGANISM: Mus
US-09-509-802-2
                                                                                                                                                  Local Simines 126;
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                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 RGLAMLDAPVSGGTAGAAAGTLTFMVGGDAEALEKARPLFEAMGRNIFHAGPDGAGQVAK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLD--QKCQNILQG--- 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 VCNNOLLAVLMIGTAEAMALGVANGLEAKVLAEIMRRSSGGNWALEVYNPWPGVMENAPA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA 550
 --EEFVDSLEKPRRILLMVKAGEA-TDKTIAALTPHLDKGDILIDGG 119
                                                        120 NTFFKDTIRRNRELSAQGFNFIGTGVSGGEEGALKGPSIMPGGQKEAYELVAPILEKIAA
                                ILAAGDRGLYEDCSSCFQAMGK
                                                                                          423 TS-----FFLGEVGNAAKMMLIVNMVQGSFMATIAEGLT-LAHVTGQSQQTLLDIL---
                                                                                                                                                   NOGOLASIFLDOKCONIL-----QGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAA
                                                                                                                                                                                 ---VILDEAANKGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.8%; Score 138.5; DB 4;
Best Local Similarity 24.3%; Pred. No. 8.1e-05;
Matches 44; Conservative 28; Mismatches 102;
                                                                                                                                                                                                               528 NEVYKRAKALDQSDNDM-----SAVYRAYI 552
                                                                                                                                                                                                                                       -----GKWTSOSSLDLGVPVTLITESVFARYI 306
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Immunex Corp.
APPLICANT: Bird, Timothy
APPLICANT: Wirca, G.D.
TITLE OF INVENTION: DEATH ASSOCIATED KIN
FILE REFERRNCE: 2889-US
CURRENT APPLICATION NUMBER: US/09/509,802
                                                                                                                                                                         240 NKGELSS-YLIEITADIFRKKDEEGNYLVD-
                                                                                                                                                                                                                                                                                RESULT 29
US-09-252-991A-29147
; Sequence 29147, Application US/09252991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09509802 Patent No. 6489130 GENERAL INFORMATION: APPLICANT: Immunex Corp.
                                  380 GRFLEAPVSGNQQLSNDGMLV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ), ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29147
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US-09-509-802-2
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                                                                                                                                                                                                                                                                                                                                                                                               KRVS-----SGSSERGSKSPLKRAQEQSPRKRGRPPKDEKDLTIPESSTVKGMMAGPMA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                             KRLSGVSSVDSAFSSRGSLS-LSFEREASTGDLG--PTD----IQKKKLVDAIISGDTS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 -LFIQEGARL-----GRIPAEVVSTCDITFACVSDPKAAKDLV--LGPSGVLQGIRPGK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              572 AWLPLHYAAWQGHLPIVKLLAKQPG-----VSVNAQ-TLDGRTPLHLAAQRGHYRVARI 624
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                                                                                                                                                                                              KVEQLKPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSE
                                                                                                                                                                                                                                          ---TFQEITSETEDLCEKPDEEVKDLAHEPGEKSSLESKSE
                                                                                                 --KIVN-----PPKDLKKPRGKKCFFVKFFGTEDHAWI
                                                Gaps
                                                Indels 189;
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     Length
Score 135.5; DB 4;
Pred. No. 0.0007;
3; Mismatches 233;
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He : 23 secs
                                                   83;
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  4.7%;
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                                                   Conservative
                                                                                                                                                                                                                                                    268 ADPQVRP-----
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OM protein - protein search, using sw model

September 16, 2004, 07:29:27; Search time 718 Seconds (without alignments) 247.335 Million cell updates/sec Run on:

US-10-067-482-2 2866 1 MAAVSLRLGDLVWGKLGRYP.....AKALDQSDNDMSAVYRAYIH

Title: Perfect score:

Sequence:

553

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1342398 seqs, 321133274 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Published_Applications_AA:* Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 4, Applia Sequence 540, Applisequence 2, Applisequence 474, Applisequence 417, Applisequence 50561, Applisequence 50561, Applisequence 174476, Sequence 2, Appli Sequence 3, Appli Sequence 417, App Sequence 1 Sequence 1 Sequence 1 Sequence 1 Description US-10-067-482-2 US-10-067-482-3 US-10-067-482-3 US-10-067-482-4 US-10-103-313-540 US-10-103-313-540 US-10-103-313-317 US-10-425-114-50561 US-10-425-114-50561 US-10-427-16 US-10-427-969-144794 US-10-427-969-144794 US-10-425-114-42840 SUMMARIES % Query Match Length D 2866 2811 2798 1279 1291 1291 1286 740.5 727 727 727 695 685 Result No.

42840, A

Sequence

Sequence 174477, Sequence 52083, A Sequence 256, App Sequence 42795, A Sequence 56894, A Sequence 151834, Sequence 57891, A Sequence 57891, A Sequence 6763, Ap Sequence 6763, Ap Sequence 6763, Ap Sequence 6781, A Sequence 6781, A Sequence 6781, A Sequence 6781, A Sequence 5206, A Sequence 5206, A Sequence 52872, A Sequence 52872, A Sequence 52872, A Sequence 52872, A Sequence 52872, A Sequence 52872, A Sequence 52872, A Sequence 52872, A Sequence 61452, A Sequence 61452, A Sequence 61452, A Sequence 61452, A Sequence 61452, A Sequence 61452, A Sequence 61452, A Sequence 61452, A Sequence 240233, Sequence 25869,	aguence 733 gquence 733 gquence 755 gquence 116 gquence 495 gquence 465 gquence 600 gquence 610 gquence 510 gquence 510 gquence 510 gquence 510	reference 2264 gruence 513, gruence 511, gruence 511, gruence 511, gruence 511, gruence 7, App gruence 14, App gruence 220, gruence 220, gruence 220, gruence 226, gruence 2486 gruence 2486 gruence 2266, gruence 51, gruence 51, gruence 51, gruence 51, gruence 51, gruence 51, gruence 51, gruence 51, gruence 51, gruence 308, gruence 51, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence 308, gruence
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481 FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQS
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Pred. No. 1.4e-230;
0; Mismatches 1;
                                                                                                        Publication US/10067482

Publication No. US20030148407A1

FEBERAL INFORMATION

APPLICANT: Origene Technologies, Inc.

TITLE OF INVENTION: Angiogenesis Dehydrogenase Gen;

TITLE OF INVENTION: Angiogenesis Dehydrogenase Gen;

CURRENT APPLICATION NUMBER: US/10/067,482

CURRENT FILING DATE: 2002-02-07

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.1

SEQ ID NO 3
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US-10-103-313-417
; Sequence 417, Application US/10103313
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Best Local Similarity
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100.0%; Score 2866; DB 14; Length 553;
Best Local Similarity 100.0%; Pred. No. 3e-235;
Matches 553; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                           APPLICANT: Origene Technologies, Inc.
TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene
FILE REFERENCE: 1U 102 R1
CURRENT APPLICATION NUMBER: US/10/067,482
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
   US-10-201-858-346
US-10-208-024-346
US-10-208-024-346
US-10-174-581-346
US-10-176-433-346
US-10-176-913-346
US-10-176-914-346
US-10-176-915-346
US-10-106-815-346
US-10-005-495A-308
US-10-013-907A-308
US-10-013-907A-308
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                                                                                                                                                                                                                                        ; Sequence 2, Application US/10067482; Publication No. US20030148407A1; GENERAL INFORMATION:
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        RESULT 1
US-10-067-482-2
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Query Match
Best Local Similarity 99.33
Matches 267; Conservative
      ; SEQ ID NO 4
; LENGTH: 276
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-482-4
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ORGANISM: Homo sapiens
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LOCATION: (4)
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US-10-103-313-540
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LENGTH: 269
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                                                                                                                                                                                                                                                                         Length 550;
Publication No. US20030082758A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PUZO7C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                        Indels
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Publication No. US20030148407A1
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc.
TITLE OF INVENTION: Angiogenesis Dehydrogenase Gene FILE REFERENCE: 10 102 R1
CURRENT APPLICATION NUMBER: US/10/067,482
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                        Score 2798; DB 14;
Pred. No. 1.9e-229;
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ilarity 98.7%;
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 543; Conserv
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US-10-067-482-4
                                                                                                                                                                    SEQ ID NO 417
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                                                                                                                                                      1 MGSGIVSNLLKWGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAA
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                                                               Gaps
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
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   Length 276;
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Publication No. US20030082758A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Frior Application removed - See File Wrapper or Palm:
SOFTWARE: Patentin Ver. 2.0
                                                            Indels
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Query Match 49.2%; Score 1410; DB 14; Best Local Similarity 100.0%; Pred. No. 1.4e-111; Matches 276; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 NHPTPMAAANEVYKRAKALDQSDNDMSAVYRAYIH 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  518 NHPTPMAAANEVYKRAKALDQSDNDMSAVYRAYIH 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.0%; Score 1404; DB 14;
99.3%; Pred. No. 4.5e-111;
tive 0; Mismatches 2;
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45.0%;
99.6%;
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Best Local Similarity 99.6'
Matches 242; Conservative
                                                              Conservative
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                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                 ICEE 244
                                                                                                                                                                                                                                                                                                                                                                                                 252 ICED 255
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US-10-425-114-50561
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US-10-103-313-474
                                                              Matches 243;
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LENGTH: 250
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                   181 PESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLKICE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD 180
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PESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLKICE 243
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US-10-103-313-474

US-10-103-313-474

Sequence 474, Application US/10103313

Publication No. US20030082758A1

SEQUENCE TO TOPORATION:

APPLICANT: ROSSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE REFERENCE: PAZO7C1

CURRENT APPLICATION NUMBER: US/10/103,313

CURRENT APPLICATION NUMBER: US/10/103,313

NUMBER OF SEQ ID NOS: 653

NUMBER OF SEQ ID NOS: 653

SOFWWARE: Patentin Ver. 2.0

SEQ ID NO 474

LENGH: 260

TYPE: PRT

CREANISM: Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 249;
                                                                                                                                                                      Sequence 2, Application US/09987755;
Publication No. US2030022312A1
GENERAL INFORMATION:
APPLICANT: Kunsch et al
TITLE OF INVENTION: Human Hepatoma-Derived Growth Factor-2;
FILE REFERENCE: FF198D1C1
CURRENT APPLICATION NUMBER: US/09/987,755
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 09/263,625
PRIOR APPLICATION NUMBER: 09/464,600
PRIOR APPLICATION NUMBER: 08/464,600
PRIOR APPLICATION NUMBER: 08/464,600
PRIOR PILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1291; DB 10;
Pred. No. 1.7e-101;
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                                                                                        241 EETGSTSIQAADSTAVNGSITPTDKKIGF 269
                                                                 244 EETGSTSIQAADSTAVNGSITPIDKKIGF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.0%;
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Matches 243; Conservative
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; ORGANISM: human
US-09-987-755-2
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                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                             72 KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRNSSEERSRP 131
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                                                                                                                                                                                                                                                                                                                                                               132 NSGDEKRKLSLSEGKVVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD
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                                                                                                                                  12 MAAVSLRIGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAMIKVEQL
                                                                                                                                                                                                              61 KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRP
                                                                                                                                                                                                                                                                                                                   121 NSGDEKRKLSLSEGKVKKNYMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKD
                                                                                                       1 MAAVSLRIGDLVWGKIGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
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  Length 260;
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US-10-103-313-317

US-10-103-317, Application US/10103313

Publication No. US20030082758A1

GENERAL INFORMATION:

APPLICANT: ROSE et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PUZ07C1

CURRENT APPLICATION UNMBER: US/10/103,313

CURRENT FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 653
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior Application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0
Score 1291; DB 14;
Pred. No. 1.8e-101;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1286; DB 14;
Pred. No. 4.6e-101;
1; Mismatches 0;
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388

61

Gaps

.. 0

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Sequence 14, Application US/10167547C
Publication No. US20030170653A1
Publication No. US20030170653A1
APPLICANT: L.1 du Pont de Nemours and Company
APPLICANT: Damude, Howard G.
TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
TITLE OF INVENTION: Butyrolactone and its Intermediates
FILE REFERENCE: CL1804 US NA
FULNERIA APPLICATION NUMBER: US/10/167,547C
CURRENT PILING DATE: 2003-03-17
RIOR APPLICATION NUMBER: 60/297198
RNDR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
                                                                                                                                                                                                                                                                                                                  269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389 GNOOLSNDGMLVILAAGDRGLYEDCSSCFOAMGKTSFFLGEVGNAAKWMLIVNWVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                    329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
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                                                                                                                                                                                                                                                              85; Indels
                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_72412C.1.pep
US-10-437-963-174476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY
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                                                                                                                                                                                                 25.4%; Score 727; DB 16; 52.1%; Pred. No. 2.7e-53; iive 49; Mismatches 85;
                                                                                                                                                                                                                                               Matches 146; Conservative
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                     TYPE: PRT ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: tulip pistil
                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local Similarity
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US-10-167-547C-14
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LENGTH: 290
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                                                                            FEATURE:
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Sequence 174476, Application US/10437963

Publication No. US20040123343A1

GENERAL INPORMATION:

APPLICANT: A Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Bunkharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT FILING DATE: 2003-05-14

SUMBER OF SEQ ID NOS: 204966

SEQ ID NO 174476
                                                                            APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 PKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNQQL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKWMLIVNWVQGSFMATIAE 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 HFHHFLLSQTEKP-AVCYQAITKK-LKICEEETGSTSIQAADSTAVNGSITPTDKKIGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 25.8%; Score 740.5; DB 12; Length 364; Best Local Similarity 47.8%; Pred. No. 2.6e-54; Matches 160; Conservative 54; Mismatches 104; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: LIB3136-019-H11_FLI.pep
US-10-425-114-50561
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Sequence 50561, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
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US-10-437-963-174476
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APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbauk, Brad
APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEO ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 KIGFLGLGLMGSGIVSNLLKWGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                                                                                                                                                                     STCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGR 381
                                                                                                                                                                                                                    FLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAARMMLIVN 441
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                                                                                                                                    34 AVTEPPARIGELGLGIMGSPMAHMLLKAGVDLTVWNRTKSKCDPLISLGAKYKPSPEEVA
                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 343;
                              Length 333,
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                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Clone ID: PAT_MRT4530_19559C.1.pep
US-10-437-963-116017
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                                                                         66
                                  DB 12;
                                  Score 682; DB 12
Pred. No. 2.2e-49
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                                                                         54; Mismatches
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                  23.8%;
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Matches 123; Conservative
                                                                             Conservative
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                                                         Similarity
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US-10-437-963-116017
US-10-424-599-144794
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                                                                             Matches 136;
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                                      Query Match
Best Local
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Publication No. US20030170653A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
APPLICANT: E.I. du Pont de Nemours and Company
APPLICANT: E.I. du Pont de Nemours and Company
APPLICANT: Damude, Howard G.
TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
TITLE OF INVENTION: Butyrolactone and its Intermediates
FILE REFERENCE: CL1804 US NA
CURRENT PILING DATE: 2003-303-17
PRICA PEPLICATION NUMBER: 60/297198
PRICA FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBENCE: 38-21(33.23.3)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 BVGFLGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVEHGASVCESPAEVIKKCKYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
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OTHER INFORMATION: Clone ID: PAT_MRT3847_101768C.1.pep
                                242 LALALGDENAVSMPVAAAANEAFKKARSLGLGDLDFSAVY
        509 LAIALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
24.2%; Score 695; DB 14;
Best Local Similarity 49.6%; Pred. No. 1.4e-50;
Matches 140; Conservative 49; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 144794, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
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ORGANISM: Arabidopsis
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                                                                                                          RESULT 12
US-10-167-547C-16
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THE KETEKENIE: BLITAKA, U344

CURRENT PEPLICATION NUMBER: U5/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR PELICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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180 TLFDVLDLGAIAN 192
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Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 52.39
Matches 101; Conservative
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                                                                                                                                                       TYPE: PRT
ORGANISM: Oryza sativa
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APPLICANT:
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APPLICANT:
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION UNDER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                        267 FSLKGPSMVKAAYPTAFPLKHQQKDLRLALALAESVSQSIPTVAAANELYKVAXSLGLAD 326
482 LDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSD 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 GARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADIVT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 VGNAAKMMLIVNWVQGSFWATIAEGLTLAHVTGQSQQTLLDIINQGQLASIFLDQKCQNI 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 LOGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYR 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 ELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGE 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: 700580946_FLI.pep
US-10-425-114-42840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Mismatches
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Sequence 174477, Application US/10437963

Publication No. US2040123343A1

SERNEAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                            Sequence 42840, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boukharov, Andrey A.
Barbazuk, Brad
Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 46.1
Matches 111; Conservative
                                                                                                                                                                                                                                                                                               APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                  542 NDMSAVYRA 550
                                                                                                                          327 ODFSAVIEA 335
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ORGANISM: Zea mays
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US-10-425-114-42840
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 174477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VLEQIGEGKGYVDMSTVDAATSCKISEAIKQKGGAFVEAPVSGSKKPAEDGQLVILAAGD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 LKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPSG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 RGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNWVQGSFWATIAEGLTLAHVTGQSQQ 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 VLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_72413C.1.pep
US-10-437-963-174477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       903
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52.3%; Pred. No. 9.9e-34;
tive 31; Mismatches 60;
                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(199)
FEATURE INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 52083, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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US-10-767-701-42795
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   83;
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 KIGFLGLGLMGSGIVSNLLKWGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 IMVGYPSDVEEVYFNDNGILNNLKPQSYVVDMTTSKPSLAKKIYAAAKERNIFALDAPVS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
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| Sequence 256, Application US/09912020
| Patent No. US20020045592A1
| GENERAL INFORMATION:
| APPLICANT: Zyskind, Judith
| APPLICANT: Trawick, John
| APPLICANT: Trawick, John
| APPLICANT: Forsyth, R. Allyn
| APPLICANT: Forsyth, R. Allyn
| APPLICANT: Forsyth, R. Allyn
| APPLICANT: Forsyth, R. Allyn
| APPLICANT: Tamancto, Robert T.
| APPLICANT: Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto, Yamancto
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER: PatentIn version 3.1
SEQ ID NO 52083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 13.1%; Score 375; DB 12; Length 292; l Similarity 30.0%; Pred. No. 2.7e-23; 85; Conservative 55; Mismatches 143; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
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Pred. No. 1.4e-22;
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Clostridium acetobutylicum
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29.4%;
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Best Local Similarity
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US-10-282-122A-52083
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US-09-912-020-256
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ORGANISM: E.
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LENGTH: 299
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Best Local S:
Matches 85
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 -NALYMGGPGAGQRAKLGNQIAIASTMVGLVEGMVYÄHKAĞLDVAKWLEAISTGAAGSKS 261
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                                                                                                                                                                      389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKAMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                       ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                                                                      187 AAMSEALTLATKAGVNPDLVYQAIRGGLAGSTVLDAKAPWVMDRNFKPGFRIDLHIKDLA 246
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                                             269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
2;
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; Pred. No. 2e-21;
54; Mismatches 145; Indels 5;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAIALGDAVNHPTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C17849_1.pep
US-10-767-701-42795
  140;
  Mismatches
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US-10-282-122A-56894
; Sequence 56894, Application US/10282122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42795, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
  57;
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     Conservative
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Best Local Similarity
Matches 86; Conserv
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PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PLING DATE: 2001-20-22

PRIOR PLING DATE: 2001-20-22

PRIOR PLING DATE: 2001-02-05

PRIOR PLING DATE: 2001-02-05

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA,034A

CURRENT APPLICATION UNDER: 105,10/282,122A

CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLILOR DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLILOR DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Enterococcus faecalis
                                         Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Publication No. US20040029129A1
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SEQ ID NO 56894
LENGTH: 296
                                                                                                                                                          Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Tou, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brobaluk, Brad
APPLICANT: Brobaluk, Brad
APPLICANT: Brobaluk, Brad
APPLICANT: Brobaluk, Brad
APPLICANT: Brobaluk, Brad
APPLICANT: Brobaluk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
KUMBER OF SEQ ID NOS: 204966
SEQ ID NO 151834
LENGTH: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFA 329
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Sequence 9081, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HEBA, TADAYOSHI
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIKAWA, HROSHI
APPLICANT: HATTORI, WSHIYIWKI
APPLICANT: SHIRA, HASOSHI
APPLICANT: SHIRA, HASOSHI
APPLICANT: SARAKI, YOSHIYWKI
APPLICANT: SHIRA, DADAYOSHI
APPLICANT: SHIRA, DADAYOSHI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151834, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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US-10-156-761-9081
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Best Local Similarity 33.08
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US-10-123-965B-11
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LENGTH: 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                      127 GALAGLAPGGLLVDMTTSDPTLAAEIAEAAAKSCAAVDAPVSGGDRGARSATLSIFAGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRGLYEDCSSCFOAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQ 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, Ĥ. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REPERRORS: ELITRA-034A CURRENT APPLICATION NUMBER: 105/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                   287 LKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAG
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                                                                                                                                                                                                                                                                                                                                     7 RSLTRRRPPLPLSAAAAAAAAAASSSATGVNVSDRPISPDTTRVAWVGTGVMGQSMAGHL
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                .
8
                                                                                                                                               Length 344;
                                                                                                                                                                                                                65; Mismatches 149; Indels
                             ; FEATURE:
*, OTHER INFORMATION: Clone ID: PAT_MRT4530_51941C.1.pep
US-10-437-963-151834
                                                                                                                                               12.1%; Score 347; DB 16; 27.5%; Pred. No. 8.6e-21;
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PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-66
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PELING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 57891, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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APPLICANT: Wang, Liangeu,
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Chlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLI
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                   84; Conservative
ORGANISM: Oryza sativa
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                                                                                                                                                     Query Match
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APPLICANT: Huang, Sheng-He TITLE OF INVENTION: B. Coli Virulence Determinants and Methods of Use Thereof File Reference: USPIGATA-SHH CURRENT APPLICATION NUMBER: US/10/123,965B CURRENT FILING DATE: 2002-12-10
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or INUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 57891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 295;
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28.8%; Pred. No. 2.7e-20;
tive 52; Mismatches 136;
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PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
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, Sequence 11, Application US/10123965B
, Publication No. US20030099966A1
, GENERAL INFORMATION:
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ORGANISM: Enterococcus faecium
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, UNN
APPLICANT: ISHIKAWA, UNN
APPLICANT: SHIKAWA, UNN
APPLICANT: SHIKAWA, UNN
APPLICANT: SHIRAY, YOSHIVUKI
APPLICANT: SHIRAY, YOSHIVUKI
APPLICANT: SHIRAY, POSHIVUKI
APPLICANT: SHIRAY, POSHIVUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL FOLYNUCLEOTIDES
FILE REPEREDENCE: 292-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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62 ISWVGYPKDVEELYLGENGFLENLAVGTVAIDMTTSSPALAKKAAEFGREKGIGVLDAPV 121
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EKIGFVGTGVMGSSMAGHLLEAGYEVLVYTRTKTKAEDLLDKGALMVETPGELANKVDIL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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.larity 27.1%; Pred. No. 1.5e-19;
Conservative 59; Mismatches 148; Indels (
                                                                                                                 243 LALENARLINTPLPNTATTQQLFSACAALGGKEWDHSALIRA 284
                                                                            LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                Sequence 60763, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-2-09
PRIOR FILING DATE: 2001-02-09
PRIOR PLILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity
Matches 77; Conserv
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                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                                                             JS-10-282-122A-60763
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US-10-282-122A-60763
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APPLICANT:
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269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/335,977
PRICATION NUMBER: US/10/335,977
PRICATION DATE: 30-Dec-2002
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
RAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature

LOCATION: (B) LCCATION 1...285

SEQUENCE DESCRIPTION: SEQ ID NO: 5655:
US-10-335-977-5655
                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GIN-018 TELECOMMUNICATION INFORMATION:
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Helicobacter pylori
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
                                                                                                                                                                     ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 285 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5655:
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQUENCES: 10031
                                                                                                                           STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
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Best Local Similarity 32...
Thes 92; Conservative
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                                                                                                                                                                                                                                                                                                 SOFTWARE: UNIX
                                                                                                   CITY: Boston
                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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US-10-282-122A-44990
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                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                       CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR PAPLICATION NUMBER: 60/203,347
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-03
PRIOR PILING DATE: 2001-12-03
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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                       Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Matches 92; Conservative
     Wall, Daniel
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APPLICANT:
APPLICANT:
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Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
                                                                                                                                                                                Yamamoto, Robert
Forsyth, R.
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Best Local Simi
Matches 74;
                                                                                                                                                                                                                                          TITLE OF INVEN
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-202
PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-66
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
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PRIOR FILING DATE: 2000-09-09
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PRIOR APPLICATION WUMBER: 60/253, 625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/267,636
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
                                                                                               Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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                                                            Zyskind, Judith
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US-10-282-122A-66301; Sequence 66301, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:

RESULT 30

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                              THILE OF INVENTION: IGENIALITICATION OF ESSENICIAL GENER IN ALCOORGAMINENES FILE OF THE TREFFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-0

PRIOR FILING DATE: 2000-05-26

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PRIOR PLING DATE: 2000-05-26

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PRIOR PLING DATE: 2001-02-06

PRIOR PRIOR DATE: 2001-02-16

PRIOR PRIOR DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLING DATE: 2001-02-16

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TION: Identification of Essential Genes in Microorganisms
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A;Map position: 4
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hor
F;40-301/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F19B15.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 18-Aug-2000
C;Accession: T08967
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G97310 dehydrogenase related to 3-hydroxyisobutyrate dehydrogenase, YKWC B. subtilis dehydrogenase related to 3-hydroxylicum c;Species: Clostridium acetobutylicum c;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                    GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                      ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                      314 GRIPAEVVSTCDITFACVSDPKAAKDLVLGP-SGVLQGIRPGKCYVDMSTVDADTVTELA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGN 432
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                                                                                                                                                           SMVTDAPDVEEVLFGENGVVKSNKRGLIFVDMSTNSPEFAKKVTKRLSEYGMEFLDAPVT 121
                                                                                                                                                                                                                                                   24 ASSTISSDIITPSNTKIGWIGTGVMGRSMCGHLIKAGYTVTVFNRTISKAQTLIDMGANV 83
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                                         269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                                                      KVGFIGLGIMGFPMASNILKAGYDLTVYNRTIEKAEKLGKMGAKVAHSPKEVAEVSEIVI
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A;Cross-references: EMBL:AL078470; GSPDB:GN00062; ATSP:F19B15.150
A;Experimental source: cultivar Columbia; BAC clone F19B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 384; DB 2; Length 334; Pred. No. 4e-18; Mismatches 152; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            242 YAMEIANSKSIPLIGTSLALQLYNAMVSLGIGELGTQGLVKVY 284
                                                                                                                                                                                                                                                                                                                                                                                               LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
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152;
    Mismatches 132;
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32.2%;
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      Conservative
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Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: DNA
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         83;
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                                                                                                                                                                                                                                                               A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: C70303
A;Statuus: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-288 <AQF>
A;Residues: 1-288 <AQF>
A;Cross=-references: GB:AE000670; NID:g2982779; PIDN:AAC06408.1; PID:g2982783; GB:AE00065
C;Genetics:
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C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Accession: G90314
R;She, Q: Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90314
A;Accession: G90314
A;Accession: G90314
A;Accession: G90314
A;Cross-references: GB:AE006641; NID:g13814790; PIDN:AAK41774.1; GSPDB:GN00155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: hibD
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
F;3-265/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                             D.E.;
                                                                                                  C70303
3-hydroxyisobutyrate dehydrogenase - Aquifex aeolicus
C;Species Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
C;Accession: C70303
R;Deckert, G: Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, V.
Nature 392, 353-358, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.7%; Score 392.5; DB 2;
larity 31.7%; Pred. No. 9e-19;
Conservative 61; Mismatches 132;
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Pred. No. 9.8e-19;
               ALIGNMENTS
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29.3%;
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Best Local Similarity
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C; Accession: G97310

C;Genetics:

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A;Map position: 68 min
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
C;Keywords: oxidoreductase
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A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-299 -KKOM>
A;Experimental source: strain K12, W3110
A;Experimental source: strain K12, W3110
A.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                 268 KKIGFLGLGLMGSGIVSNILKMGHTVTVWNRTABKCDLFIQEGARLGRTPABVVSTCDIT 327
                                                                                                                                                                                                                                                                                                   328 FACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPV 387
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                                                                                                                                                                                                                                                                                                                                                               63 ITMVGYPSDVEEVYFGSNGIIENAKEGAYLIDMTTSKPSLAKKIAEAAKEKALFALDAPV
                                                                                                                                                                                                           SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 MIGVAEAMAYAQKSGLEPENVLKSITTGAAGSWSLSNLAPRMLQGNFEPGFYVKHFIXDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 MATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) homolog - Escherichia co
N;Alternate names: hypothetical 31K protein (rnpB-sohA intergenic region)
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA
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                                                 Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 RLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAYI 552
                                   12.8%; Score 368; DB 2; Length 28 26.7%; Pred. No. 3.8e-17; Live 65; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.8%; Score 367; DB 1; Length 299
29.4%; Pred. No. 4.7e-17;
Live 57; Mismatches 140; Indels
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                               Query Match
Best Local Similarity
Matches 76; Conserv
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Matches 83; Conserv
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C;Species: Bacillus subtilis
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R'Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A; Reference number: A96900; MUID:21359325, PMID:21359325
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
F;5-266/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE001437; PIDN:AAK81274.1; PID:915026424; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.1%; Score 375; DB 2; Length 29 Similarity 30.0%; Pred. No. 1.3e-17; Similarity 55; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
                                                                                                                                                                                                                                                                              A;Residues: 1-292 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-288 <KUN>
                                                                                                                                                                        A, Accession: G97310
A, Status: preliminary
                                                                                                                                                                                                                                           A; Molecule type: DNA
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Best Local Simi.
Matches 85;
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coli (strain K-12)

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A,Gene: yhaE
C,Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
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C.Species: Salmonella enterica subsp. enterica serovar Typhi
A.Note: this species has also been called Salmonella typhi
A.Note: this species has also been called Salmonella typhi
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C.Accession: AE0897
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connetton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulle, S.; O'Gaora, P.
Nature 413, 448-852, 2001
A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; MuID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AL513382; PIDN:CAD07771.1; PID:g16504320; GSPDB:GN00176
C;Genetics:
A;Gene: garR
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hc
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                             449 ATIAEGITLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 AAMSEALTLATKAGVNPDLVYQAIRGGLAGSTVLDAKAPMVMDRNFKPGFRIDLHIKDLA 246
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                                                                            Length 299;
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1 Similarity 28.7%; Pred. No. 1.1e-16;
80; Conservative 58; Mismatches 141; Indels
                                                                       Similarity 29.4%; Score 367; DB 2; Length 29
Similarity 29.4%; Pred. No. 4.7e-17;
33; Conservative 57; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 NALDTSHGVGAQLPLTAAVMEMMQALRADGLGTADHSALACY 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAIALGDAVNHPTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
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A,Molecule type: DNA
A,Residues: 1-294 <PAR>
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Best Local
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C; Genetics
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A) Residues: 1-299 cSTO>
A) Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                     substrain RIMD
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                       ATIAEGLILAHVIGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                              187 AAMSEALTLATKAGVNPDLVYQAIRGGLAGSTVLDAKAPMVMDRNFKPGFRIDLHIKDLA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 29.4%; Pred. No. 4.7e-17;
Matches 83; Conservative 57; Mismatches 140; Indels
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hor
C;Keywords: oxidoreductase
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F;7-268/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: AL035478; PIDN: CAB36613.1; GSPDB: GN00070; SCOEDB: SC2G5.26c
                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNA--AKM---ML 438
                                                                                                                                                                                                                                                                                                                                                               324 CDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFL 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable dehydrogenase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Accession: T34659
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajand
submitted to the EMBL Data Library, February 1999
A;Reference number: 221559
A;Accession: T34859
                                                                                                                                                                                                                                                                                 62 ADFVFACIGNDDDLRSVIVGADGAFSIMKKDAIFIDNITASAEVARELDKEAQKRGFHFM
                                                                                                                                                                                                                                       266 TDKKIGFLGLGLMGSGIVSNL-LKMGHTVTVWNRTAEKCDLFIQE-GARLGRTPAEVVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 IVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDF
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                                                                                                                                                                                      Gaps
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                                                                                                                     Length 291;
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                                                                                                                                                                                   Indels
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                                                                                                           11.7%; Score 335; DB 2; L 27.3%; Pred. No. 6e-15; ive 65; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                          Query Match
Best Local Similarity 27.20
Local Similarity 27.20
Local 79; Conservative
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Best Local Similarity 28.69
Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                     C;Accession: S76381
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C.Superfamily: 3-hydroxy1sobutyrate dehydrogenase; 3-hydroxy1sobutyrate dehydrogenase hq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) - Synechocystis sp. (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLG----RTPAEVVSTC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 DITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLE 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 APVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQ 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                           C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Keywords: oxidoreductase
;6-267/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Match 11.8%; Score 338; DB 2; Length 290; Local Similarity 29.6%; Pred. No. 3.8e-15; les 85; Conservative 50; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 KDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reference number: 874322; MUID:97061201; PMID:8905231
                                             C;Species: Synechocystis sp. A;Variety: PCC 6803
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A,Residues: 1-291 <KUR>
A,Cross-references: GB:
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A,Status: preliminary
A,Molecule type: DNA
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A; Status: preliminary
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C;Genetics:
A;Gene: BMEI1024
A;Map position: I
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Best Local S:
Matches 85
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Addroxyisobutyrate dehydrogenase (B. subtilis YkwC protein) homolog lmol005 [imported] 3-hydroxyisobutyrate dehydrogenes (C.Species: Listeria monocytogenes (C.Species: Listeria monocytogenes (C.Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 (C.Accession: AE1200 (C.Accession: AE1200 (C.Accession: AE1200 (C.Accession: AE1200 (C.) Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H., S.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Science 294, 849-852) (Sci
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
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A;Residues: 1-286 <GLA>
A;Residues: 1-286 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99083.1; PID:g16410407; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Gametics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 QAVLGECYLFVEKAGVDPAIAYEIIKRSAGFSKSMEWSVDAILDRAFDPRFSINLLHKDI 242
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268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT 327
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Best Local Similarity 27.1%; Pred. No. 1.1e-14;
Matches 77; Conservative 59; Mismatches 148; Indels
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3-hydroxytsobutyrate dehydrogenase BH2634 [imported] - Bacillus halodurans (strain C-125 3-hydroxytsobutyrate dehydrogenase BH2634 [imported] - Bacillus halodurans (species: Bacillus halodurans C;Species: Bacillus halodurans C;Species: Dacids Basillus halodurans C;Accession: B83979
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83979
A;Accession: B83979
A;Accession: B83979
A;Residues: 1-299 <STO>A;Residues: 1-299 <STO>A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06353.1; GSPDB:GN00
A;Reperimental source: strain C-125
C;Genetics:
A;Gene: BH2634
                                                                               Julydroxyisobutyrate dehydrogenase (B. subtilis YkwC protein) homolog lin1004 [imported] C; Species: Listeria innocus C; Species: Listeria innocus C; Decies: Listeria innocus C; Decies: Listeria innocus C; Decies: Z7-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C; Date: Z7-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C; Deciesion: AC1558 R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker C; Domiquez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A; Kunn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mahand, A.; Aller Comparative genomics of Listeria species.

A; Althe: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AC1558

A; Status: preliminary
A; Mesidues: 1-286 < GLA>
A; Accession: AC158
A; Cross-references: GB:AL592022; PIDN:CAC96235.1; PID:g16413463; GSPDB:GN00178
A; Experimental source: strain Clip11262
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSF 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ISWYGYPKDVEQLYLGENGFLDNLKAGSVAIDWTTSSPALAKKIAEAGHEKGIGVLDAPV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 FACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGDIGAKNGTLAIMVGGAEDVFLKVKPIFEILGSSVILQGDAGSGQHTKMVNQIAIAŠN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 75; Conserv
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Best Local S:
Matches 84
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hypothetical protein NWA1773 [imported] - Neisseria meningitidis (strain 22491 serogroup CySpecies: Neisseria meningitidis (cySpecies: Desagnor CySpecies: Nay-2000 #sequence_revision 05-May-2000 #text_change 09-Nov-2001 Rysatkhill. J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell Alloroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000 Asquence of a serogroup A strain of Neisseria menigitidis 22491. A;Reference number: A81775; MuID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: NWA1773
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
F;9-266/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-289 <PAR>
A;Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85001.1; PID:g7380415
A;Experimental source: serogroup A, strain Z2491
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     269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
                                                                                                                329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
                                                                                                                                                   68 LMVSDYAAVCDIL---NGVRDGL-AGKIIVNMSTISPTENLAVKALVEAAGGGFAEAPVS 123
                                                                                                                                                                                                                                389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                     124 GSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFHFGDVGKGSGAKLVLNSLLGIFG 183
                                                                                                                                                                                                                                                                                                                                             449 ATIAEGLTLAHVIGOSQOTLLDIINQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
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                                      probable 3-hydroxyisobutyrate dehydrogenase PA1576 [imported] - Pseudomonas
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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Best Local Similarity
Matches 84; Conserv
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CiSpecies: Neisseria meningitidis
CiSpecies: Neisseria meningitidis
CiSpecies: Neisseria meningitidis
Cipacession: B81065
Strettelin, H: Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; H. din, H: Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
              Avariety: strain Joseph Print.

Avariety: strain Joseph Print.

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

C;Accession: GJD, Lo.S. Lo.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: G71912

A;Accession: G71912

A;Accession: Foreliminary

A;Accession: L295 <ARN>
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Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: jhp0585
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
F;3-260/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
;9-266/Pomain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TMLSD-KAAIDAVLAPKFWEQMSK--KIVVNMSTIAPLESLSLEKIAQKHQATYLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 ATIAEGLTLAHVTGQSQQTLLDIINQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.5%; Score 330; DB 2; Length 285; 32.7%; Pred. No. 1.2e-14; Indels ive 46; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                         A, Experimental source: strain J99 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: AE001491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92; Conservative
C;Species: Helicobacter pylori
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Matches 92; Conserv
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Molecule type: DNA
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A;Status: preliminar
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C;Accession: fi83456
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, i. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Complete génome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathos
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 csTO-
A;Cross-references: GB:AE004579; GB:AE004091; NID:g9947455; PIDN:AAG04889.1; GSPDB:GN001:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: PA1500
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Debigs train dehydrogenase (ABO15439) [imported] - Agrobacterium tumefaciens (strain C58, C; Species: Agrobacterium tumefaciens (strain C58, C; Species: Agrobacterium tumefaciens c; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C; Date: 22-Oct-2001 #sequence_revision 2.Oct-2001 #text_change 18-Nov-2002 C; Accession: Agrass R; R; C; Cattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable oxidoreductase PA1500 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                206 LNGLSEGLMLAEQAGLDIPNLVACLKNGAAGSWOMENRALTMSQEKFDFGFAIDWMIKDL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLLVNMVQGSF 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGEVGAKAATLSIMVGGCPNTFERALPLFQAMGKNITRVGGNGDGQTAKVANQIIVALN 181
                                                              86 LTCVGNDDDVRSMTTAATGAIPAMKPGAVLIDHTTTSALLAEELSAAAQQAGLHFMDAPV 145
                                                                                                                                    SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSF 447
328 FACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Species: Pseudomonas aeruginosa
C,Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KIGFIGTGIMGKPMAQNLQKAGHSLFLSTHHDAAPADL-LEAGAIALANPKEVAQEAEFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 KIGFLGLGLMGSGIVSNLLKMGHTVTV-WNRTAEKCDLFIQEGARLGRIPAEVVSTCDIT
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                                                                                                                                                                                                                                                                               448 MATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDL
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                                                                                                                                                                                                                                                                                                                                                                                                                              508 RLAIALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVYRA 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
11.1%; Score 318; DB 2; Lo
Best Local Similarity 29.0%; Pred. No. 8.2e-14;
Matches 83; Conservative 51; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388
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           C;Accession: F83447

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradan, S.J.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.J. Lim, J. Lory, S.; Olson, M.V.

Mature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Status: preliminary

A;Status: preliminary

A;Status: DNA

A;Nolecule type: DNA

A;Residues: 1-288 <5TO>
A;Cross-references: GB:AE004586; GB:AE004091; NID:g9947536; PIDN:AAG04965.1; GSPDB:GN001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.3%; Score 324.5; DB 2; Length
larity 26.5%; Pred. No. 2.9e-14;
Conservative 62; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                509 LAIALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAV 547
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llarity 26.9%; Pred. No. 8.3e-14;
Conservative 52; Mismatches 154;
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Best Local Similarity
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nes 76; Conserv
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A;Title: Genome Sequence of the plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A98338
A;Accession: A98338
A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-315 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK90227.1; PID:g15160240; GSPDB:GN00170
C;Genetics:
A;Gene: AGR L. 3303
A;Gene: AGR L. 3303
A;Map position: linear chromosome
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-hydroxyisobutyrate dehydrogenase mmsB [imported] - Agrobacterium tumefaciens (strain c'species: Agrobacterium tumefaciens
C'species: Agrobacterium tumefaciens
C'species: Agrobacterium tumefaciens
C'Accession: Al2944
R'Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Remero, P.; Zhang, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A.Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                  268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT 327
                                                                                                                                                                                                                                                                                                                                                                                                        387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: GB:AE008689; PIDN:AAL43975.1; PID:g17741531; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT 327
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                                                                                                                                                                                                                                        11.1%; Score 318; DB 2; Length 315; 27.0%; Pred. No. 9e-14; Live 58; Mismatches 139; Indels
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Best Local Similarity 27.0%; Pred. No. 9e-14;
Matches 75; Conservative 58; Mismatches 139;
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ses 75; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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Matches
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hypothetical protein ywjF [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssy
A;Reference number: A86625; MUID:2135186; PMID:11337471
A;Status: preliminary
A;Residues: L293 <STO>
A;Residues: L-293 <STO>
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C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hom
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SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSF 447
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A;Experimental source: strain IL1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 ILVGYPKDVREVYFGAEGIFKNDCSGKVLIDMTTTEPTLAQEIYQEAKKVGAFALDAPVS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 GGDLGAKNATLTIMVGGDSETYEKALPLFEKNGKTITHQGAVGSGQHTKMANQICIAGTM 182
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A;Experimental source: cultivar Columbia; BAC clone T13K14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 316; DB 2; Length 29; Pred. No. 1.1e-13; 48; Mismatches 143; Indels
                                                                                                                                                                                                                                                             508 RLAIALGDAVNHPTPMAAAANEVYKR-----AKALDQS
                                                                                                                                                                                                                                                                                                                              STALAFAKSRGLSLPVGEEVDRLFRSMVEHGAGELDHS
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27.9%;
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Best Local Similarity 27.9%;
Conservative
74; Conservative
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A; Residues: 1-371 <BEV>
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449 ATIAEGLTLAHVTGQSQQTLLDI-LNQGQLASIFLDQKCQNIL-
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Matches 74; Conserv
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C82323
A;Status: preliminary
A;Accession: C82323
A;Status: preliminary
A;Accession: C82323
C;Status: preliminary
A;Accession: C82332
C;Gratics: A;Residues: 1-296 cSTO>
A;Cross-references: GB:AE004753; GB:AE004091; NID:g9949433; PIDN:AAG06700.1; GSPDB:GN001
C;Genetics:
A;Gene: PA3312
C;Superfamily: 3-hydroxvisohutvrare Arthurances
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                                      A;Map position: 4
A;Introns: 38/3; 68/2; 106/3; 157/1; 208/3; 240/3; 288/2; 316/3; 343/2
A;Introns: 38/3; 68/2; 106/3; 157/1; 208/3; 240/3; 288/2; 316/3; 343/2
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase homology <HIB>
F;40-344/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 TSEALALGQSLGISASTLTEVLNTSSGRCWSSDAYNPVPGVMKGVPSSRDYNGGFASKLM 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
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                                                                                                                                                                                                                                                                                 QEGARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQG---IRPGKCYVDMSTVD
                                                                                                                                                                                                                                                                                                                                                                                           137 PQTTRKISLAVSNCNLKEKRASFCSSCEQVEIVSFSLVSSIFDVDNWEKPVMLDAPVSGG
                                                                                                                                                                                                      248 STSIQAADSTAVNGSITPIDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI
                                                                                                                                                                                                                                         SGSLHRFSSSSQNSN---QFQNVGFIGLGNMGFRMVNNLIRAGYKVTVHDINRDVMKMFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAEGLTLAHVTGQSQQTLLDILN--QGQLASIFLDQKCQNILQG-----NFKPDFYLKYI
                                                                                                                                                                    Gaps
                                                                                                                                                                      48;
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                                                                                                                             Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY
                                                                                                                           Score 316; DB 2; Length 37;
Pred. No. 1.5e-13;
58; Mismatches 154; Indels
                                                                                                                                   11.0%;
25.3%;
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                                        Similarity
                  A; Gene: ATSP:T13K14.90
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                                                                                                                                   Query Match
Best Local S:
Matches 88
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probable 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) [imported] - Sinorhizobium me C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 A;File The complete sequence of the 1,683-Kb pSymb megaplasmid from the N2-fixing endo A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
Science 293, 668-672, 2001
Abduthors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A,Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A,Gontents: annotation
C,Genetics:
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A,Genome: plasmid
C,Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
C,Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 GEVGAKNASLSIMAGGKPSSFERALPLFKLMGKNITLVGDCGDGQVTKVANQIIVALTIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 IVACNALVIAEVVALAERAGVDASLVAPALAGGFADSKPLQILAPQMAESRYEPVKWHVR
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0
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                                                                             502 YIQKDLRLAIALGDAVNHPTPWAAAANEVYKRAKALDQSDNDMSAVYRAY
                                                                                                                     10.8%; Score 309; DB 2; Length 29 26.3%; Pred. No. 3.2e-13; rive 53; Mismatches 154; Indels
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Discosion: B96736

Cispecies: Arabidopsis thaliana (mouse-ear cress)

Cispecies: Arabidopsis thaliana (mouse-ear cress)

Cispecies: Arabidopsis thaliana (mouse-ear cress)

Cispecies: Arabidopsis thaliana (mouse-ear cress)

Cispecies: Arabidopsis thaliana (mouse-ear cress)

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                                                                                                                                                                                61 IMVPDIPQVEEVLEGENGCTKASLKGKTIVDMSSISPIETKRFARQVNELGGDYLDAPVS 120
                                                                                                                                                                                                                                                                               GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                           449 ATIAEGLTLAHVTGOSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 BAVSEALLFASKAGADPVRVRQALMGGFASSRILEVHGERMIKRTFNPGFKIALHQKDLN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 ITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005173; NID:g6714326; PIDN:AAF26019.1; GSPDB:GN00141
                         329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
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Best Local Similarity 28.33,
Thes 76; Conservative
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A,Molecule type: DNA
A,Residues: 1-297 <STO>
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General SWb20668
A;Genome: plasmid
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase ho
                                                                                                                                                                        A; Molecule Type: DNA
A; Residues: 1-301 < KUR.
A; Residues: 1-301 < KUR.
A; Residues: 1-301 < KUR.
A; Residues: 1-301 < KUR.
A; Experimental source: strain 1021, megaplasmid pSymB
B; Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Science 293, 668-672, 2001
L; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Ahathors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Worg, K.; Yeh, K. A; Title: The composite genome of the legume symbiont Sinorhizoblum meliloti.
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A;Cross-references: GB:AE000157; GB:U00096; NID:g1786716; PIDN:AAC73611.1; PID:g1786719;
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase hc
F;3-263/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>
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Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A,Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing
A,Reference number: A95842; MUID:21396508; PMID:11481431
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A, Status: preliminary; nucleic acid sequence not shown; translation not
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A; Reference number: A64720; MUID: 97426617; PMID: 9278503
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                                                                                                                                                                                                                                                                                                                                                 REDLINE=98044013; Pubmed=9384377;

RA KUNDE FP, Oggaswara N., Moszer I., Albertini A.M., Alloni G.,

RA KUNDE P., Oggaswara N., Moszer I., Albertini A.M., Borchert S.,

RA Macwedo V., Bertero M.G., Beseirese P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

R. Broullet S. Brusshi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Guiseppi G., Guy B.J., Haga K., Hairodo C.R., Henaut A.,

RA Guiseppi G., Guy B.J., Haga K., Hairodo C.R., Henaut A.,

RA Guiseppi G., Guy B.J., Haga K., Hairodo C.R., Mones L.,

RA Guiseppi G., Guy B.J., Haga K., Hairodo C.R., Krandh G.,

RA Milbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kobaysshi Y., Koetter P., Koningstein G., Krandh S., Kumano M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Parro V., Pohl T.M., Potretelle B., Rapoport G., Rey M., Reynolds S.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

Sekiguchi J., Sekowska A., Seror S., Shin B.S., Soldo B.,

Sato T., Scanlan E., Schleich S., Schroeter R., Yoshian S., Vanacholl M., Yanane K., Yasawuchti A.,

Takeuchi M., Tamakoshi A., Tanaka T., Tarpstra P., Tognoni A.,

Voshida K., Yoshikawa H.F., Zumktein E., Yoshikawa H., Danchin A.,

RA Yoshida K., Yoshikawa H.F., Zumktein E., Yoshikawa H., Danchin A.,

RA H. Harkollis W., Wasarotti M., Panachin R., Hantils R., Haller R., Waller R.,
                                                                                                                                                                                                                                                         "Sequence of the Bacillus subtilis chromosome from ykuA to cse-15."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997).
-i- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                        Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                       10-0CT-2003 (Rel. 36, Last sequence update)
Hypothetical oxidoreductase ykwC (EC 1.1.-.)
YKWC OR BSU13960.
                   288 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z99111; CAB13269.1; -.
PIR; B69870; B69870.
Subtiliat; BG13328; VkwC.
InterPro; IPR002204; 3hydroxisobut_dh
InterPro; IPR006183; 6PGD.
InterPro; IPR006183; 6PGD.
PAGM; PR006184; 6PGD. NAD.
PRINTS; PR00616; 6FGDDHDRGNĀSE.
                                                                                                                                                                                                                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
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                                                     Created)
                                                                                                                                                                                                                                STRAIN=168;
Scanlan E., Devine K.M.;
                       STANDARD;
                                                     (Rel. 36, (Rel. 36, 1) (Rel. 36, 1)
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                          Bacillus subtilis
                                                                                                                                                                            NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATIABGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKY1QKDL 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 MIGVAEAMAYAQKSGLEPENVLKSITTGAAGSWSLSNLAPRMLQGNFEPGFYVKHFIKDM 242
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MEDLINE-22388234; PubMed=12471157;
MEDLINE-22388234; PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Melch R.A., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T. Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coll.",
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Komine Y., Inokuchi H.; "Precise mapping of the rnpB gene encoding the RNA component of RNase P in Escherichia coli K-12.";
                                                                                                                                                                                                            268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT
                                                                                                                                                                                                                                          SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSF
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992;
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28-FEB-2003 (Rel. 41, Last annotation update)
2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tartronate
Hypothetical protein; Oxidoreductase; NAD; Complete proteome
                                                                                                      Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAYI 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 GIALEEABLMGEEMPGLSLAKSLYDKLAAQGBENSGTQSIYKLWV 287
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                                                                                                   ; Score 368; DB 1; Length 28; Pred. No. 3.2e-16; 65; Mismatches 144; Indels
                                                    976DD9098DB47A30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 AA
                                 BY SIMILARITY
                                                                                                              12.8%; Score 368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91154140; PubMed=1705543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               semialdehyde reductase) (TSAR).
GARR OR B3125 OR C3880.
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30-MAY-2000 (Rel. 39, Last seq
                                                    288 AA; 30711 MW;
                                                                                                                                          26.78;
                                                                                                                                                                   76; Conservative
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                                                                                                                    Query Match
Best Local Similarity
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                                   ACT SITE
SEQUENCE
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P23523;
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Y229 SYNY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 AAMSEALTLATKAGVNPDLVYQAIRGGLAGSTVLDAKAPMVMDRNFKPGFRIDLHIKDLA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 TMLPNSPHVKEVALGENGIIEGAKPGTVLIDMSSIAPLASREISEALKAKGIDMLDAPVS 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTBLAQVIVSRGGRFLEAPVS
                                                                                                                                        MEDLINE=20225875; PubMed=10762278; Monterrubio R., Baldoma L., Obradors N., Aguilar J., Badia J.; Monterrubio R., Baldoma L., Obradors N., Aguilar J., Badia J.; A common regulator for the operons encoding the enzymes involved in B-galactarate, D-glucarate, and D-glycerate utilization in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
                                        Hubbard B.K., Koch M., Palmer D.R., Babbitt P.C., Gerlt J.A., "Evolution of enzymatic activities in the enolase superfamily: characterization of the (D)-glucarate/galactarate catabolic pathway
                                                                                                                                                                                                                                    oxopropanoate + NAD(P)H.
-!- PATHWAY: D-galactarate metabolism; third step.
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                          J. Bacteriol. 182:2672-2674 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.8%; Score 367; DB 1; Length 29 29.4%; Pred. No. 3.8e-16; ive 57; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               509 LAIALGDAVNHPTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
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                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EcoGene; EG11176; garR.
InterPro; IPR002204; Jhydroxisobut_dh.
InterPro; IPR006183; 6PGD.
InterPro; IPR006185; 6PGD.NAD.
InterPro; IPR006398; Tartro sem_red.
Pfam; PP03446; NAD binding_2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, D90012; BAA14238.1; ALT_INIT.
EMBL, U18997; AAA57228.1; ALT_INIT.
EMBL, AE000394; AAC76159.1; ALT_INIT.
EMBL, AE016767; AAN82321.1; ALT_INIT.
                                                                                  in Escherichia coli.";
Biochemistry 37:14369-14375(1998).
                              MEDLINE=98447507; PubMed=9772162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 AA; 30427 MW;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 KIAVFGLGVMGSPMAQNLVKNGYQTVGYNRTLERPS--VQEAAKAGVKVVTSIAVAAANA
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mt region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
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PIK; 9763B1, 2763B1.
InterPro; IPR002194; 3hydroxisobut_dh.
InterPro; IPR006183; 6PGD.
InterPro; IPR006118; 6PGD.
InterPro; IPR006118; 6PGD MAD.
Pfam; PF03446; NAD. binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
PROSTIE; PS00895; 3 HYDROXYISOBUT DH; 1.
HYPOCHELICAI protein; Oxidoxeductase; NAD; Complete proteome.
ACT_SITE 175 HYPOSTIES BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.8%; Score 338; DB 1; Length 29 29.6%; Pred. No. 2.5e-14; ive 50; Mismatches 144; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 KDLRLVREA--AENGPLPGVTLAESLFTSVQLLGGEDQGSQAIIRAY
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                                                                                                                                                                                                                                                      Bacteria; Cyanobacteria; Chroccoccales; Synechocystis.
                                                        is-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase SIr0229 (EC 1.1.-.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Æ
                                                                                                                                                                                                                           (strain PCC 6803)
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Q9SUCO; Q8LC25;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 AA; 29930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                    Synechocystis sp.
                                                                                                                                                                                                                                                                                    NCBI_TaxID=1148;
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A MEDLINES-2008348HE FURNGETINGER.

RA MEDLINES-2008348HE FURNGETINGERTHER.

RA MEDLINES-2008348HE FURNGERTH SIGNER R., MURDIN, C., VOICKGERT G., RALFER R., DUSCETCHOEFT A., SCHOELLER R., RIGGER M., BOLLY M., RIGGER M., MELIER M., DESTEND M., BATTERS B., AMSORGE W., BY PART R. P. OF STRONGER M., BOULTY M., BATTER T., RECHART B., POTTER L. ZIMMERTAND M., WEGLER H., RALGEY P., SARGONN, BOULTY M., BATTER T., DEFOOT E., RAGONNER S., A., MCCALIGAB B., BILDAM L., ROODEN J., AMGONIAN S.-A., MCCALIGAB B., BILDAM L., ROODEN J., AMGONIAN S.-A., MCCALIGAB B., BILDAM L., ROODEN J., AMGONIAN S.-A., MCCALIGAB B., BILDAM L., ROODEN J., AMGONIAN R., BATTER R., DEFOOT E., WELZENGER M., WELLE R., BEAUN M., MELTER H., BEAUN M., MELTER H., BEAUN M., MELTER H., BEAUN M., MCAPALLER S., VAN AND DELE R., JAMENDER S., VAN MONIGON W., VAN KOOPERS J., VAN MONIGON M., SCOPER P., SCHEN F., AMGONIAN S., MAYSE R., AMGONIAN S., MAYSE R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., LANDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PELDER R., PERCHER R., PELDER R., PELDER R., PERCHER R., SCHMICH W., LECHARTHY A., ANDOURT S., ROMEND S., PERCHER R., SCHMICH W., LECHARTHY A., ANDOURT S., SCHMAD S., PERCHER R., SCHMAD S., HILLER R., SCHMAT S., SCHMICH W., LECHARTHY A., ANDOURT S., SCHMAD S., PERCHER R., SCHMAT S., SCHMICH W., LECHARTHY R., SCHMAD S., PERCHER R., SCHMAD S., PERCHER R., SCHMAD S., PERCHER R., SCHMAT S., SCHMICH R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER R., MARCHER
             10-OCT-2003 (Rel. 42, Last annotation update)
Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor
                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Bmbryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Spermatophyta; Magnoliophyta; Erassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methyl-3-oxopropanoate + NADH.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Full-length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Troukhan M., Alexandrov N., Lu Y.-P., Flavell
10-OCT-2003 (Rel. 42, Last sequence update)
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-20083488; PubMed=10617198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 402:769-777(1999).
                                                                               AT4G20930 OR T13K14.90
                                                           (EC 1.1.1.31) (HIBADH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                      eurosids II; Bra:
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brover V., Tro
Feldmann K.A.;
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-!- CAUTION: Ref.1 sequences differ from that shown due to erroneous

gene model prediction.

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9
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                                                                                                                         noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 QEGARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQG---IRPGKCYVDMSTVD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 ADTVTELAQVIVSRGGR-----FLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCS 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474 -QGQLASIFLDQKCQNILQG-----NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 SSGRCWSSDAYNPVPGVMKGVPSSRDYNGGFASKLMAKDLNLAAASAEEVGHKSPLISKA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77
                                           between the Swiss Institute of Bioinformatics and the EMBL outstatt
the Buropean Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSLHRFSSSSQNSN---QFQNVGFIGLGNMGFRMVNNLIRAGYKVTVHDINRDVMKMFT
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STRAIN=K12 / MG1655;
MEDLINE=9742667; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE 3-HYDROXYISOBUTYRATE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                     InterPro; IPR002204; 3hydroxisobut dh.
PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
Transit peptide.

34 MITOCHONDRION (BY SIMILARITY)
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 154; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEDZE87CC3DE191C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
S -> F (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 328; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 35, Last sequence update) (Rel. 42, Last annotation update)
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                                                                                                                                                            entities requires a license agreement (Gor send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 QEIYKKMCEEGHETKDFSCVFRHF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEVYKRAKALDOSDNDMSAVYRAY 551
                                                                                                                                                                                                                                          EMBL; ALO80282; CAB45888.1; ALT_SEQ.
EMBL; AL161554; CAB79093.1; ALT_SEQ.
EMBL; AY086845; AAM63893.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
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347 AA; 37364 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.2%;
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219
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10-OCT-2003
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CONFLICT
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ACT SITE
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P77161;
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241 LALOSAKALALNLPNTATCQELFNTCAANGGSQLDHSALVQA 282

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 IMVPDTPQVEEVLFGENGCTKASLKGKTIVDMSSISPIETKRFARQVNELGGDYLDAPVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 BAVSEALLFASKAGADPVRVRQALMGGFASSRILEVHGERMIKRTFNPGFKIALHQKDLN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KLGFIGLGIMGTPMAINLARAGHQLHV-TTIGPVADELLSLGAVSVETARQVTEASDIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                   Cusa E., Obradors N., Baldoma L., Badia J., Aguilar J.;
"Genetic analysis of a chromosomal region containing genes required
for assimilation of allantoin nitrogen and linked glyoxylate
metabolism in Escherichia coli.";
J. Bacteriol. 181:7479-7484(1999).
-!- CAPALYTIC ACTIVITY: (R)-91ycerate + NAD(P) (+) = 2-hydroxy-3-
                                                                                        SEQUENCE FROM N.A.

Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
Submitted (JAN-1897) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                           -!- INDUCTION: By glyoxylate.
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
  Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.5%; Score 301.5; DB 1; Length 292; 27.7%; Pred. No. 4.8e-12; Indels 1; ve 51; Mismatches 152; Indels 1;
                                        sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5D5263231F2910F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PINE D64782; D64782.

BCOGENE; EG13265; glxR.
INTERPRO; IRRO02204; BryCroxisobut_dh.
INTERPRO; IRRO06183; GFGD.NAD.
INTERPRO; IRRO06183; GFGD.NAD.
INTERPRO; IRRO06183; GFGD.NAD.
INTERPRO; IRRO06398; TATITO sem_red.
PRINTS; PRO0076; GFGDHDRGNASE.
TIGRRAMS; TIGRRAMS; TATICO sem_red; I.PROSITE; PS00895; 3 HYDROXTISOBUT DH; I.OXidoreductase; NAD; COMPlete profesome.
ACT_SITE 169 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Glyoxylate catabolism.
-!- INDUCTION: By glyoxylate.
                                                                                                                                                                                                                                                MEDLINE=20069628; PubMed=10601204;
                                                                                                                                                                                                              SEQUENCE FROM N.A., AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000157; AAC73611.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30800 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U89279; AAB93851.1; -.
                                      "The complete genome sequenc
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                       oxopropanoate + NAD(P)H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 27.78
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 AA;
                                                                                                                                                                                                                                  STRAIN=K12 / ECL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family.
  Gregor J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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MEDLINE-22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Atlausner R.D., Collins F.S., Magner L., Sheamen C.M., Schuler G.D.,

Atlausner R.D., Collins F.S., Magner L., Sheamen C.M., Schuler G.D.,

Atlachul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusdina K., Farmer A.A., Rubin G.M., Hong L.,

Boardsein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Carninci P., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Muzny D.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.W., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.W., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                     RANGULINE EXTRINGATION ORGAN;
RAY SEQUENCE FROW N.Y.
RAY GARAZAKI TISSUE—0lfactory organ;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osaton N., Salto R., Suzuki H., Yamanaka II., Kiyosawa H.,
RA Nikaido I., Osaton N., Salto R., Suzuki H., Yamanaka II., Kiyosawa H.,
RA Galarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Fazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Marchionni L., Mockenzie L., Miki H.,
RA Maglott D.R., Maltais L., Marchionni L., Mockenzie L., Miki H.,
RA Magshima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Ravasi T., Reed D.C., Reed D.J., Raid B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Numata K., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Wilming D.G., Wynshaw-Boris A., Yanagisawa M., Yang I.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hara A., Hashizume W., Imotani K., Ishin Y., Litoh M., Kagawa I.,
RA Shiraki T., Waki K., Sasaki D., Shibata K., Shinagawa A.,
Ranishino A., Yanashizaki Y., Itoh M., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor (EC 1.1.1.31) (HIBADH).
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                           335 AA.
                                                      STANDARD;
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                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                 DH3I MOUSE
Q99LI3; Q8BJY2;
                                                                                                                                                                                                                         HIBADH.
RESULT 6
DH3I_MOUSE
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36
39
208
68
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SEQUENCE
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MUTAGEN
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ACT SITE
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                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 VSKELÄKEVEKMGAVFMDAPVSGGVGAARSGNLTFNVGGVEDEFAAAQELLECMGSNVVY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 IQEGARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDAD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427 LGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILN--QGQLASIFLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 CGAVGTGQSAKICNNMLLAISMIGTAEAMNLGIRSGLDPKLLAKILNMSSGRCWSSDTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCQNILQG-----NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 TVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSLAAVCSRSMA---SKTP----VGFIGLGNMGNPMAKNLMKHGYPLILYDVFPDVCKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Gaps
                                                                                   SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-HYDROXYISOBUTYRATE DEHYDROGENASE.
    CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC.1992 (Rel. 24, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3-Apdroxyisobutyrate dehydrogenase, mitochondrial precursor HEBADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; NAD; Mitochondrion; Transit peptide.
TRANSIT 1 35 MITOCHONDRION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAD (ADP PART) (POTENTIAL)
                                                               similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A -> S (IN REF. 1).
SE9ECB03997DB110 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.4%; Score 297; DB 1; 26.1%; Pred. No. 1.1e-11;
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                                                               (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1889802; 6430402H10Rik.
INCERPRO; IPR002204; 3hydroxisobut_dh.
INCERPRO; IPR0061183; 6PGD.
INCERPRO; IPR006118; 6PGD.
Ffan; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
PROSITE; PS00895; 3_HYDROXXISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00895; 3_HYDROXYISOBUT_DH; 1.
                       methyl-3-oxopropanoate + NADH.
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                EMBL; BC003914; AAH03914.1; -. EMBL; AK078175; BAC37162.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 AA; 35440 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | |:|::
SKKDFSSVFQ 327
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67
208
                                                                                                                                                                                                                                                                                                                                                       PIR; PT0534; PT0534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81;
                                                                                                            family
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P29266;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 IQBGARLGRIPABVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDAD 366
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-!- TISSUE SPECIFICITY: HIGHER LEVEL IN KIDNEY, LIVER, AND HEART THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEDLINE=96335606; PubMed=8766712;
Hawes J.W., Harper E.T., Crabb D.W., Harris R.A.;
"Structural and mechanistic similarities of 6-phosphogluconate and 3-
hydroxyisobutyrate dehydrogenases reveal a new enzyme family, the 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D-XR: DECREASE OF ACTIVITY WITH NAD,
INCREASE OF ACTIVITY WITH NADE.
K->A,H,N,R: COMPLETE LOSS OF ACTIVITY.
Y-Q: DECREASE IN ACTIVITY.
D266A7838S00295A CRC64;
                                                                                                                                                                                                                                          Rougraff P.M., Zhang B. Kuntz M.J., Harris R.A., Crabb D.W.;
"Cloning and sequence analysis of a cDNA for 3-hydroxyisobutyrate
dehydrogenase. Evidence for its evolutionary relationship to other
pyridine nucleotide-dependent dehydrogenases.";
J. Biol. Chem. 264:5899-5903(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the 3-hydroxyisobutyrate dehydrogenase
bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSTIE: PS00895; 3 HYDROXYISOBUT DH; 1.

Oxidoreductase; NAD, Mitochondrion; Transit peptide.

TRANSIT 1 35 MITOCHONDRION (BY SIMILARITY).

CHAIN 36 33 3-HYDROXYISOBUTRATE DEHYDROGENASE.

NP BIND 39 67 NAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bairoch A.;
Unpublished observations (JAN-2001).
-!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CAUTION: Ref.1 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157; Indels
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25.5%; Pred. No. 3e-11;
cive 60; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A32867; A32867.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006183; 6FGD.
InterPro; IPR006115; 6FGD.NAD.
Pfam; PF0346; NAD binding_2: 1.
PRINTS; PR00076; 6FGDBDRGNASE.
PROSITE; PS00895; 3_HYDROXISOBUT_DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE
                                                                                                                                                                                                TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J04628; AAA50312.1; ALT_FRAME
                                                                                                                                                                                                STRAIN=Sprague-Dawley; TISSUE=Live
MEDLINE=89174651; PubMed=2647728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methyl-3-oxopropanoate + NADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     frameshift in position 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydroxyacid dehydrogenases.";
FEBS Lett. 389:263-267(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs
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212
335 AA;
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                                                                                                                                                                      SECUENCE FROM N.A.
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us-10-067-482-2.rsp

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NCBI_TaxID=562, 623;
                Similarity
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ID YIHU ECOLI
Query Match
Best Local S:
Matches 72
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         TVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFF 426
                                                                                   484
                                                                                                             198 CGAVGSGOSAKICNNMLLAISMIGTAEAMNLGIRSGLDPKLLAKILNMSSGRCWSSDTYN 257
                                                                                                                                               485 KCQNILQG----NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQ 539
                                                                                                                                                                       258 PVPGVMDGVPSSNNYQGGFGTTLMAKDLGLAQDSATSTKTPILLGSVAHQIYRNMCSKGY 317
                                       138 VSKELAKEVEKMGAVFMDAPVSGGVGAARSCHLTFMVGCVENEFAAAQELLGCMGSNVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krogan N.J., Zhang R., Neuhard J., Kelln R.A.,
"Utilization of dihydroorotate as sole pyrimidine source by Salmonella
                                                                              LGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILN--QGQLASIFLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-155 4948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Waterston R., Wilson R.K., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
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Stydene; SG7????; yihU.

Stydene; SG7???; yihU.

InterPro; IPR002204; 3hydroxisobut_dh.

InterPro; IPR00215; 6FGD_NAD.

InterPro; IPR00205; 3hydroxisobut_dh.

InterPro; IPR00205; 3hydroxisobut_dh. 1.

PR03IIE; PS00895; 3hydroxisobut_dh. 1.

PROSIIE; PS00895; 3hydroxisobuteise; NAD; Complete proteome.

Hypothetical protein; Oxidoreductase; NAD;

STRE 171 171

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
YPPCthetical oxidoreductase yihU (EC 1.1.-.)
YIHU OR STM4023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF220438; AAF27921.1; -.
EMBL; AE008887; AAL22862.1; -.
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                      540 SDNDMSAVYR 549
                                                                                                                                                                                                                                                       318 SKKDFSSVFQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=LT2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          typhimurium.";
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                                                                                                                                                             330 CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSG 389
                                                                                                                                                                                         184 LSAEAAVLCEALGLSFDVALKVMSGTAAGKGHFTTTWPNK----VMKGDLSPAFMIDLAH 239
                                                                                                                                                                                                                                                                                4 IAFIGLGOMGSPWASNLLKOGHOLSVFDVNPDAVQRLVDKGAQPASSPAQATIGAEFVIT
                                                                                                                                                                                                                                             390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA
                                                                                                                                                                                                                                                                                                                               450 TIAEGLTLAHVTGQSQQTLLDILN----QGQLASIFLDQKCQNILQGNFKPDFYLKYIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=S.flexneri; STRAIN=301 / Serotype 2a; MEDLINE=22272406; PubMed=12384590; Jin W., Wang J., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           flexheri serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786(2003).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
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                                             9,
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SPECIES=E.coli, STRAIN=K12 / MG1655,
MEDLINR=3347969; PubMed=8346018;
Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
"Analysis of the Escharichia coli genome. III. DNA sequence of region from 87.2 to 89.2 minutes.";
Nucleic Acids Res. 21:3391-3398(1993).
      DB 1; Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete genome sequence and comparative genomics of Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a; MEDLINE=22590274; PubMed=12704152;
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   505 KDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV 547
                                                                                                                                                                                                                                                                                                                                                                                                                                       240 KDLGIALDVANQLHVPMPLGAASREVYNLARAAGRGREDWSAI 282
10.1%; Score 289.5; DB 1; 25.4%; Pred. No. 2.8e-11; ive 59; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P32142;
01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypotherical oxidoreductase yinu (EC 1.1.-.)
XIHU OR B3882 OR SF3954 OR S3792.
Escherichia coli, and
                     1 Similarity 25.4%; 72; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 IGFIGLGLMGSGIVSNILLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 LSAEAAVLCEALNLPFDVAVKVMS-GTAAGKGHFTTSWPNKVLSGDLSPAFMIDLAHKDL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLBAPVSG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 MLPNGDLVRNVLFGENGVCEGLSTDALVIDMSTIHPLQTDKLIADMQAKGFSMMDVPVGR 123
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 TIAEGLTLAHVTGQSQQTLLDILNQGQLA--SIFLDQKCQNILQGNFKPDFYLKYIQKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFWA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         э;
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBLY, A40826; S40826.

PIR; $40826; S40826.

Exceller, EG11847; yihU.

InterPro; IPR002204; 3hydroxisobut_dh.

InterPro; IPR006115; 6PGD_NAD.

Pfam; PF03446; NAD binding 2; 1.

PROSITE; PS00895; 3 HYDROXYISOBUT_DH; 1.

PROSITE; PS00895; 0xidoreductase; NAD; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P31937; Q9UDN3;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
3-hydroxyisobutyate dehydrogenase, mitochondrial precursor
(EC 1.1.1.31) (HIBADH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74FBC8C09FA7881C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508 RLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.0%; Score 287.5; DB 1 26.4%; Pred. No. 3.7e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Oxidoreductase; NAD; ACT SITE 171 171 BY SIMILARITY SEQUENCE 298 AA; 31158 MW; 74FBC8C09FA
                                                                                                                                                                                                                                                                                                                                   EMBL; AE000464; AAD13444.1; -. EMBL; AE015402; AAN45389.1; -. EMBL; AE016990; AAP18811.1; -.
                                                                                                                                                                                                                                                                                                      EMBL; L19201; AAB03015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 26.4%;
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 GARLGRIPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADIVT 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005739; C:mitochondrion; NAS.
GO; GO:0008442; F:3-hydroxylabobutyrate dehydrogenase activity; NAS.
GO; GO:0006573; P:valine metabolism; NAS.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006483; GFGD.
InterPro; IPR006418; GFGD.
Pfam; PP03446; NAD_binding_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBBRIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sanchez J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-HYDROXYISOBUTYRATE DEHYDROGENASE. NAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94147969; PubMed=8313870;
Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C
Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
"Human liver protein map. update 1993.";
Electrophoresis 14:1216-1222(1993).
-:- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.8%; Score 281; DB 1; Length 336; 26.4%; Pred. No. 1.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Du F., Wohldmann P., Holmes A.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DA3128774A91AF48 CRC64;
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Oxidoreductase; NAD; Mitochondrion; Transit peptide.
TRANSIT 36 MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                            Sci. U.S.A. 99:16899-16903(2002)
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Siena-2DPAGE; P31937; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC032324; AAH32324.1; --
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PROSITE; PS00895; 3_HYDROXYISC
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                                                                                                                                                                                                                                                                                                                                                                                                                  OF 32-336 FROM N.A.
                                                                                                                                                                                                                                                                                                                          cDNA sequences."
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209
336 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 37-47.
                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236795;
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MIM; 23679
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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RA MAGNETIME STOROGY, PubMed=10731132;

RA MAGNETIME-2196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., LiD P.W., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., LiD P.W., Hoskins R.A., Galle R.F.,

RA GACOGER R.A., Lewis S.E., Richards S., Ashburner M., Handerson S.N.,

RA Gutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Barlon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbaran A., Baxendell G., Relzen C.R., Miklos G.L.G.,

RA Abril J.F., Agbaran A., Baxendell G., Relzen C.R., Miklos G.L.G.,

RA Abril V.F., Baune P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Ballew R.M., Canley S., Dallke C., Davenport L.B., Dothakov S.,

RA Burtis R.C., Busam D.A., Buller H., Cadiue B., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Buller C., Perrara C., Ferriera S., Fleischmann W.,

RA Bartis N.L., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Googer C., Gabrielian A.E., Gaary N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F. Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwan C.,

RA Glodek A., Gong F. Gorrell J.H., Gu Z., Kennison J.A., Kechum K.A.,

RA Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,

Alali M., Kalush F., Karpen G.H., Li Z., Liang Y., Moshrefi A.,

Andali M., Kalush F., Karpen G.H., Li Z., Liang Y., Melson D.L.,

RA Merkulov G., Milshian N.V., Mobarry C., Morris J., Moshrefi A.,

RA Helson D.R., Petteman G.S., Pan S., Pollard U., Puri, V., Rese M.G.,

RA Belazzolo M., Pittman G.S., Pan S., Pollard U., Puri, W. Mag X.,

RA Belazzolo M., Pittman G.S., Pan S., Pollard U., Puri, W. Mag X.,

RA Spier E., Spradling A.C., Stapleton M., Stuese B., Swith T.,

RA Spier E., Spradling A.C., Stapleton M., Stuese B.,

RA Wells S.M., Woodes T.W., Wooder C., Wu D., Yang S., Yao, Q.A.,

RA Shens R., Tector C., Turner R., Venter E., Wang A., W., Smith H.O.,

RA Shens R., Tector C., Turner R., Wenter E., Wang S., Yang S., Rulb D.,

RA Shen
               ELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGE 429
                                                        430 VGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILN--QGQLASIFLDQKCQ 487
                                                                                                                                                                                                                          202 VGTGQAAKICNNMLLAISMIGTAEAMNLGIRLGLDPKLLAKILNMSSGRCWSSDTYNPVP 261
                                                                                                                                                                                                                                                                                                  488 NILQG-----NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDN 542
                                                                                                                                                                                                                                                                                                                                               Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EC 1.1.1.31) (HIBADH).
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322 DFSSVFQ 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 DMSAVYR 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9V8MS; Q9V8M6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 FACVSD---PKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKGARFIDAPVSGGVPGAEQATLTFWVGGTEAEYNAŸKAVL
ECMGKKITHCGVYGMGQAAKLCNNMALAISMIGVSEAMNLA
VRQGLDANVF -> KCRQGRPRVHGQEDHPLRRLWHGPGRQ
                                                                                                MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D. M.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
NAIVDASYDEMTADGVNKDTIFIDSSTISPDLVKSLQKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVQQHDAGHLDDRCFGGHESGGAPGSRCQCLRRDHQLLHRT
LLGLGDLQPCARSLPQCPSQQGLRRRFLLGSDHQGSGSGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 KNIGFVGLGNMGANMASNLIKAGHKLHVFDISKPACDGLAAKGATVYAKTSELAKNSDFV
                                                                                                                                                                                                                                                                                                                                                                                                                 = 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9V8MS-2; Sequence=VSP 001281, VSP 001282; SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGORFQLTHPAGISGAQGLPVAVR (in isoform
                                                                                                                                                                                                                                                                                                                   "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                      Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.7%; Score 278.5; DB 1; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MITOCHONDRION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROBABLE 3-HYDROXYISOBUTYRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBg10034330; CG15093.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD. NAD.
PRINTS; PR00066; 6PGDHDRGNAGE.
PROSITE; PR000695; 3HYDROXISOBUT_DH; 1.
PROSITE; PR00895; 3HYDROXISOBUT_DH; 1.
Transit peptide; Alternative splicing.
TRANSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                               methyl-3-oxopropanoate + NADH.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity)
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAD (ADP PART) (POTENTIAL).
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A39B534753EAE83E CRC64;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 1.5e-10; 47; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTIG=VSP 001281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9V8M5-1; Sequence=Displayed;
                                                                            AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003798; AAF57638.2; -. EMBL; AE003798; AAM68444.1; -.
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324
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196
227
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                                                                                                                                                                                                                                                                                                                                                     systematic review.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Long;
                                                                                                                                                                                                                                                                                                Lewis S.E.;
                                                                         REVISIONS
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Oxidoreductase; NAD; Complete proteome.
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                                                                                                                                                                                                                     GSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKC----QNILQG----- 492
                                                                                               APVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQ 444
                                                                                                                                                                                                                                                                         204 AISMIGVSEAMNLAVRQELDANVFAEIINSS-----TGRCWASEIYNPVPGVCPSAPA 256
   144 APVSGGVPGAEQATLTFMVGGTEAEYNAVKAVLECMGKKITHCGVYGMGQAAKLCNNMML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20437337; PubMed=10984043; Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steele M.I., Lorenz D., Hatter K., Park A., Sokatch J.R.; "Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO encoding methylmalonate-semialdehyde dehydrogenase and 3-
                                                                                                                                                                                                                                                                                                                                                  --NFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      = 2-
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-!- PATHWAY: Distral valine metabolic pathway.
-!- INDUCTION: By valine
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
10-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) (HIBADH)
MMSB OR PA3569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 AA
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PIR, C42902, C42902.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006115, 6PGD_NAD.
Pfam; PF03446, NAD binding 2; 1.
PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydroxyi sobutyrate dehydrogenase.";
J. Biol. Chem. 267:13585-13592(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-92317087; PubMed=1339433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M84911; AAA25892.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=287;
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PSEAE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFA 329
                                                                                                                                                                                                                        330 CVSDPKAAKDIVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSG 389
                                                                                                                                                                                                                                                64 MLPAGGHVESLYLGDDGLLARVAGKPLLIDCSTIAPETARKVAEAAAAKGLTLDAPVSG 123
                                                                                                                                                                                                                                                                                                      449
                                                                                                                                                                                                                                                                                                                                     124 GVGGARAĞTLSFIVGGPAEGFARARPVLENMĞRNIFHAĞDHĞAĞQVAKICNNMLLĞILMA 183
                                                                                                                                                                                                                                                                                                                                                                             450 TIAEGLTLAHVTGQSQQTLLDILNQ---GQLA-----SIFLDQKCQNILQGNFKPDF 498
                                                                                                                                                                                    63
                                                                                                                                                                        4 IAFLGLGNMGGPMAANLLKAGHRVNVFDLQPKAVLGLVEQGAQGADSALQCCEGAEVVIS
                                                                                                                                                                                                                                                                                                    NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 499 YLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDN--DMSAVYRAY 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      = 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) = 2. methyl-3-oxopropanoate + NADH.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                             17;
                                                                       Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial
(EC 1.1.1.31) (HIBADH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WormPep; B0250.5; CE18481.
InterPro; IPR002204; 3hydroxisobut dh.
INTER, PS00895; 3. HYDROXYISOBUT DH; 1.
Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.
NP_BIND 2 ND NAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lloyd C., White S.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                             Indels
                                   0C4D7B5A7C870730 CRC64;
                                                                                       pred. No. 1.6e-09;
51; Mismatches 151;
                                                                         DB 1;
NAD (BY SIMILARITY).
BY SIMILARITY.
                                                                           Score 261.5; DB 1
Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 AA
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EMBL, AL031630; CAB21003'1; --
EMBL, 281453; CAA21003.1; JOINED.
PIR; T18682; T18682.
                                     298 AA; 30486 MW;
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                                                                           9.1%;
                                                                                             Local Similarıtı
nes 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                     171
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Similarity
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                                                                                                            271 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFAC 330
                                                                                                                                                                            331 VSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGN 390
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                                                                                                                                                                                                                                           ----QQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNWVQGS 446
                                                                                                                                                                                                                                                                                                        447 FWATIAEGLTLAHVTGOSQQTLLDILN--------QGQLASIFLDQKCQNILQ 491
                                                                                                                                                                                                                                                               182 OMVAVAETMNLGISMGLDAKALAGİVNTSSGRCWSSDTYNPVPGVIENİ---PSCRGYAG 238
                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                      492 GNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYK-RAKALDQSDNDMSAVYR 549
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5 GFIGLGNMGCHMARNLIKNGKKLIVYDVNKAVVQEFKAEGCEVAAHPADIAAASKEIITV
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                     31;
                                                   Score 259.5; DB 1; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000357; AAC75778.1; -.
PIR; D65054; D65054.
EcoGene; E013104; ygbJ.
InterPro; IPR0022204; Mydroxisobut dh.
PROSITE; PS00895; HYDROXISOBUT DH; 1.
Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
ACT_SITE 178 BY SIMILARITY.
                                                                                 48; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
 172 172 PROBABLE.
299 AA; 31217 MW; F30B423A597CABF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09E94256EDDFC26C CRC64;
                                                                    2.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Hypothetical oxidoreductase ygbJ (EC 1.1...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 AA.
                                                                    Pred. No.
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MEDLINE-97426617; PubMed-9278503;
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                                                9.1%;
                                                               25.8%;
                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562;
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                                             Query Match
Best Local Simil
Matches 77; (
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SEQUENCE
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Length 302;

8.3%; Score 239; DB 1;

Query Match

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                                                                                                                                                                                                                                                                                                          61 AEKLDALLVLVVNAAQVKQVLFGETGVAQHLKPGTAVWVSSTIASADAQEIATALAGFDL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 VSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGG 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                               440 VNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFY
                                                                                                                                                                                                                                                                                                                                                                                                     381 RFLEAPVSGNOOLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLG-EVGNAAKMMLI
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MEDLINE=22064494; PubMed=12218036,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Praser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=9925937 PubMed=1874210;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Biglaneier K., Gas S., Barry C.B. III. Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Comor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
Nature 393:537-544(1998).
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16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last amnotation update)
Probable 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) (HIBADH)
MMSB OR RV0751C OR MT0775 OR MTV041.25C OR MB0773C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                          Indels
22.9%; Pred. No. 4.1e-08;
live 64; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=M.tuberculosis; STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Bacteriol. 184:5479-5490(2002).
                                  67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                     methyl-3-oxopropanoate + NADH.
PATHWAY: Distal valine metabolic pathway.
SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                          ., Nařl. Acad. Sci. Ú.S.A. 100.7877-7882(2003).
CATALYTIC ACTIVITY: 3-hydroxy-2-methylpropanoate + NAD(+) =
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BY SIMILARITY.
       complete genome sequence of Mycobacterium bovis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Hypothetical oxidoreductase yfjR (EC 1.1.--) YFJR OR BSU07990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002204; 3hydroxisobut dh. PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1. Oxidoreductase; NAD; Complete proteome.
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74; Conservative
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TIGR; MT0775; -.
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                                                                                                                                                                                                                              REDINES 98044033; PubMed=9384377;

KUNDELINE-98044033; PubMed=9384377;

RA Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Berganel S.C., Broon S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterbfet A., Edhlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Guiseppi G., Guy B.J., Haga K., Haicot J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Guiseppi G., Guy B.J., Haga K., Haicot J., Harwood C.R., Henaut A.,

A Coris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Xiein C.,

RA Kutita K., Lapidus A., Liut H., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Noone D., Pohl T.M., Portetelle D., Porwollik S., Resyonic G., Rey M., Reynolds S.,

RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Sekiguchi J., Sekowska A., Seros S.J., Serror P., Shin B.S.,

RA Serothi A., Tanaka T., Takahashi H., Takemaru K.,

RA Tasato V., Uchiyama S., Vandenbol M., Vannier F., Vasaarotti A.,

RA Tosato V., Wohlkawa H.F., Zumstein E., Woeller H., Wanters P., Wipat A., Yamamoco H., Yamane K., Yashilasa H., Panchina A., Wanbuti R., Wedler E., Wedler H., Yamane C., Vasaarotti A.,

RA Viari A., Wanbutt R., Wander E., Wedler H., Vannier P., Danchin A.,

RA Viari A., Wanbutt R., Wander E., Wedler H., Yannier V., Yashikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.P., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.P., Zumstein E., Yoshikawa H.P., Zumstein E., Valla M., A., Zumstein E., Wander E., Walla M., 
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Subtilist; BG12914; YfjR.
Interpro; IPR002204; 3hydroxisobut_dh.
PROSTIR; PS008905; 3 HYDROXXISOBUT DH; FALSE NEG.
Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
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ve 51; Mismatches 133; Indels
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                                        Microbiology 142:3057-3065(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997)
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121 AKPLLDSLSQQIFDVGEESKTANAAK--ISINFLLVSMLEALSESFLMMEKYGLEQKQFL 178
                                      470 DILNQGQLASIFLDQKCQN----ILQGNFKP-DFYLKYIQKDLRLAIALGDAVNHPTPMA 524
                                                                          179 EI----ASALFGSPVYÖNYGTIMAEQKFEPAGFKMSLGLKDINLALAAAKRVSANLPLA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98295897; PubMed=9634230; Carnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Stelton S., Squares S., Squares R., Secjevic M., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22206494; PubMed=12218036; Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Rollonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002204; 3hydroxisobut dh.
PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
Hypothetical protein; Oxidoreductaes; NAD; Complete proteome.
ACT_SITE 176 176 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical oxidoreductase Rv0770/MT0794 (EC 1.1.-.-).
RV0770 OR MT0794 OR MTCY369.15.
                                                                                                                                                                                                                                                                        295 AA
                                                                                                                      525 AAANEVYKRAKALDQSDNDMSAVYR 549
                                                                                                                                                 234 ELAKSHFESGIEKGFGDLDWAALIK 258
                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1773;
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BY SIMILARITY.
7A9E7FBFAD0E95B8 CRC64;

295 AA; 30445 MW;

ACT SITE SEQUENCE

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                                                                     265 PTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTC 324
                                                                                                                                                                   445 GSFMATIAEGLTLAHVTGQSQQTLLDILNQGQL------ASIFLDQKCQNILQG 492
                                                                                                                                           325 DITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLE 384
                                                                                                                                                                                                              385 APVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQ 444
                                                                                                                                                                                                                                                                                                                     184 FVSYAAAAEAQRLAEACG-----LDLVALGKVVRHSDSFTGGAGAIMFRNTTAPMEPAD 237
                                                                                                                63
                                                                                             "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                          25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Relischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 269:496-512(1995).
Science 269:496-512(1995).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
         Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006115; 6PGD NAD.
Pfam: PF03446; NAD binding_2; 1.
PROSITE; PS00895; 3 HYDROXXISOBUT DH; 1.
Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
                                          Indels
                                                                                                                                                                                                                                                                                                                                                        493 NFKPDFYLKYI----QKDLRLAIALGDAVNHPTPMAAAA 527
                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                    l Similarity 24.7%; Pred. No. 2.8e-06;
69; Conservative 48; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical oxidoreductase HI1010 (EC 1.1.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 AA
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(Rel. 34, Last sequence update)
(Rel. 42, Last annotation update
     7.3%; Score 209.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U32782; AAC22671.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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              Similarity
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Query Match
Best Local
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                                  Matches
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X KRANI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Rarawa T., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Gasavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalow S., Casavant T.,

Radota K., Matsudi F., Gissi C., King B., Kochiwa H.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullita M., Maria M., Lee N.H.,

A Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
                                                                                                                                                        388
                                                                                                                                                                                                              447
                                                                                                270 IGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGAR-LGRTPAEVVSTCDITF 328
                                                                                                                                                                                                                              507
                                                                                                                                                                                                                                                                                          188 IAAGAEAMALASKAGIPLDVMYDVVTNAAGNSWMFENRWKHVVEGDYTPLSMVDIFVKDL 247
                                                                                                                           67
                                                                                                                          8 VAVIGLGSNGNGAAVSCINAGLTTYGIDLNPVALEKLKAAGAKAVAANGYDFAHELDAVV
                                                                                                                                                       329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                        GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLG-EVGNAAKMMLIVNMVQGSF
                                                                                                                                                                                                                                                                   MATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDL
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE=97445118; PubMed=9299445; Izumoto Y., Nakamura H.; Izumoto Y., Kuroda T., Harada H., Kishimoto T., Nakamura H.; Hepatoma-derived growth factor belongs to a gene family in mice showing significant homology in the amino terminus."; Biochem. Biophys. Res. Commun. 238:26-32(1997).
                                                                        5
                                             Length 301;
                                                                                                                                                                                                                                                                                                                                           248 GLVNDTAKSLHFPLHLASTAYSMFTEASNAGYGKEDDSAVIKIF 291
                                                                                                                                                                                                                                                                                                                           508 RLAIALGDAVNHPTPMAAANEVYKRAKALDOSDNDMSAVYRAY 551
                                          ; Score 198; DB 1; Length 30; Pred. No. 1.5e-05; 62; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao Y., Chen W., Mang Y., "Cloning of novel gene related to thymus development.", Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                 7C615A25B0947D18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PS1859; Q9CYA4; Q9JK87;
01-OCT-1996 (Rel. 34, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HDGF OR TDRM1.
    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/c; TISSUE-Testis;
                    31035 MW;
                                              6.9%;
                                                                           59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
       177 1
301 AA;
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                                                 Query Match
Best Local Similarity
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        ACT SITE
SEQUENCE
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                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                      Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.5%; Score 186.5; DB 1; Length 237; 29.8%; Pred. No. 5.8e-05;
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P -> H (IN REF. 1).
Q -> P (IN REF. 1).
AAE4CF574DA4733F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI 1194494; Hdgf.
InterPro; IPR000313; PWWP_domain.
Pfam; PF00855; PWWP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50812; PWWP; 1.
Growth factor; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF251787, AAF65469.1; --
EMBL, AK017063; BAB30979.1; --
EMBL, BC005713; AAH05713.1; --
EMBL, BC021654; AAH1654.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
190
229
                                                                                    Nature 409:685-690(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 2
237 AA;
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118
190
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Matches 6
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STANDARD;
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              HUMAN
                                       P51858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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KEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSSDDKNRRNSSEERSRPNSGDEK 126
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                                                                 70 KEKFGKPNKRKGFSEGLWEIEN----NPTVKASGYQSSQKKSCAAEPEVEPEAHEGDGD 124
                                                                                                                                         127 RKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKR----AQEQSPRKRGRPPK----D 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gordon E.H.J., Pike A.D., Hill A.E., Cuthbertson P.M., Chapman S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification and characterization of a novel cytochrome c3 from Shewanella frigidimarina that is involved in Fe(III) respiration.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. J. 349:153-158 (2000).
-!- SIMILARITY: Belongs to the 3-hydroxyisobutyrate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical oxidoreductase in cytochrome c3 5'region (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
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                                                                                                                                                                                                                                                                            178 EKDLTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADP 215
                                                                                                                                                                                                                                                                                                                                             177 EED---KEIAALEGERPLPVEVEK-NSTPSEPDSGQGP 210
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26.3%; Pred. No. 5.2e-05;
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es 51; Conservative
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RESULT 21 HDGF_HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hepatoma-derived growth factor (HDGF) (High-mobility group protein 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura H., Izumoto Y., Kambe H., Kuroda T., Mori T., Kawamura K., Yamamoto H., Kishimoto T., "Molecular cloning of complementary DNA for a novel human hepatomaderived growth factor. Its homology with high mobility group-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: Heparin-binding protein, with mitogenic activity for
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A. 99:16899-16903 (2002)
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G0; G0:0005737; C:cytoplasm; TAS.
G0; G0:0005615; C:extracellular space; TAS.
G0; G0:0008201; F:heparin binding; TAS.
G0; G0:0008283; P:cell proliferation; TAS.
InterPro; IPRO00313; PWWP_domain.
PFam: PF00855; PWWP; 1.
SMART; SM00293; PWWP; 1.
PROSITE; PS50812; PWWP; 1.
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 4-24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Contains 1 PWWP domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 269:25143-25149(1994).
                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Hepatoma;
MEDLINE=95014294; PubMed=7929202;
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PIR; A55055; A55055.
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                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                              like 2) (HMG-1L2).
HDGF OR HMG1L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                        99
                                                                                                                              69
                                                                                                        7 RLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHAH
                                                                                                                                                                             KEKFGKPNKRKGFSEGLWEIEN----NPTVKASGYOSSOKKSCVEEPEPEAEGDGD
                                                                                                                             KCGDLVFAKMKGÝPHWPARIDEMPBAAVKSTANK-YQVFFFGTHETAFLGPKDLFPYEES
                                                                                                                                                                                                    RKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPLKRAQ----EQSPR--KRGRPPKDEKD
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                            (G/T)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANT GLY-39.
Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P., Nguyen D.A., Livingston R.J., Poel C.L., Robertson P.D., Schackwitz W.S., Shravood J.K., Witrak L.A., Nickerson D.A.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95327934; PubMed=7604265;
Palombo F., Gallinari P., Iaccarino I., Lettieri T., Hughes M., D'Arrigo A., Truong O., Hsuan J.J., Jiricny J.;
"GTBP, a 160-Kilodalton protein essential for mismatch-binding activity in human cells.";
Science 268:1912-1914(1995).
                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=97098445; PubMed=8942985;
Acharya S., Wilson T., Gradia S., Kane M.F., Guerrette S.,
Marsischky G.T., Kolodner R.D., Fishel R.;
"hMSH2 forms specific mispair-binding complexes with hMSH3 and
                                                                                                                                                                                                                                                                                                                                  MSH6 HUMAN STANDARD; PRT; 1360 AA.
P52701; 043706; 043917; QBTCX4;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
DNA mismatch repair protein MSH6 (MutS-alpha 160 kDa subunit)
                                                            Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=98116665; PubMed=9455487;
Shiwaku H.O., Wakatenki S., Mori Y., Fukushige S., Horii A.;
"Alternative splicing of GTBP in normal human tissues.";
DNA Res. 4:359-362(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-116 FROM N.A., AND VARIANT GLY-39.
MEDLINE=96435440; PubMed=8838326;
Nicolaides N.C., Palombo F., Kinzler K.W., Vogelstein B.,
                                                                                  Indels
                       223 POLY-GLU.
26788 MW; DD60D9203BDD4B34 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 93:13629-13634(1996).
                                                            DB 1;
                                                                                  30; Mismatches 100;
                                                                                                                                                                                                                                                                         ---KEAATLEVERPLPMEVEK-NSTPSEPGSGRGP 210
                                                                                                                                                                                                                                                                                                                                                                                                       (GTMBP) (P160).
                                                                                                                                                                                                                                                  LIIPESSTVKGMMAGPMAAFKWQPIASEPVKDADP 215
                                                           Score 185.5; DB 1
Pred. No. 6.8e-05;
           PWWP.
                                                                                                                                                                                                                                                                                                                                                                                                   mismatch binding protein) (GTBP)
 Growth factor; Heparin-binding.
DOMAIN 12 69 PW
                                                         6.5%;
                                                                                   64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                    240 AA;
                                                                        Similarity
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                                       SEQUENCE
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Best Local
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MEDLINE=95127935; PubMed=7664266; Papadopoulos N., Nicolaides N.C., Liu B., Parsons R., Lengauer C., Palombo F., D'Arrigo A., Markowitz S., Willson J.K.V., Kinzler K.W., Jiricny J., Vogelstein B.; The Markowitz S., Willson J.K.V., Kinzler K.W., Whutations of GTBP in genetically unstable cells."; Science 268:1915-1917(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Association of hereditary nonpolyposis colorectal cancer-related tumors displaying low microsatellite instability with MSH6 germline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miyaki M., Konishi M., Tanaka K., Kikuchi-Yanoshita R., Muraoka M.,
Yasuno M., Igari T., Koike M., Chiba M., Mori T.;
"Germline mutation of MSH6 as the cause of hereditary nonpolyposis
                                                                                                                                                                                         Drummond J.T., Li G.-M., Longley M.J., Modrich P.; "Isolation of an hMSH2-pl60 heterodimer that restores DNA mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS CRC ILE-285; ARG-566; GLY-803 AND THR-1087, AND VARIANTS GLY-39; ASP-220; VAL-396 AND LEU-800.
MEDLINE=20005667; PubMed=10537275;
Kolodner R.D., Tytell J.D., Schmeits J.L., Kane M.F., Gupta R.D., Weger J., Mahlberg S., Pot E.A., Peel D., Ziogas A., Garber J.E., Syngal S., Anton-Culver H., Li F.P.;
"Germ-line msh6 mutations in colorectal cancer families.";
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Wang Q., Lasset C., Desseigne F., Saurin J.-C., Maugard C.,
Navarro C., Ruano E., Descos L., Trillet-Lenoir V., Bosset J.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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MEDLINE=21666030; PubMed=11807791;
Plaschke J., Krueger S., Pistorius S., Theissig F., Saeger H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21470348; PubMed=11586295; Wensink R.G.J., Verlind B Wu Y., Berends M.J.W., Sijmons R.H., Mensink R.G.J., Verlind E Kooi K.A., van der Zee A.G.J., Kempinga C., van der Zee A.G.J., Hellema H., Buys C. C.H.C.M., Kleibenker J.H., Hofstra R.M.W.; "A role for MLH3 in hereditary nonpolyposis colorectal cancer."
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20245492; PubMed=10783165;
Wang Y., Cortez D., Yazdi P., Neff N., Elledge S.J., Qin J.;
"BASC, a super complex of BCR1-associated proteins involved
recognition and repair of aberrant DNA structures.";
Genes Dev. 14:927-939(2000).
"Molecular cloning of the N-terminus of GTBP."; Genomics 31:395-397\,(1996).
                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION OF MSH6 AS MEMBER OF BASC.
                                                                                                                         CHARACTERIZATION, AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Hum. Genet. 65:1291-1298(1999)
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MEDLINE=99452590; PubMed=10521294;
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                                                                                                                                                             PubMed=7604264;
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                                                                                                                                                                                                                                                                                      repair to tumor cells.";
Science 268:1909-1912(1995).
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                                                                                                                                                                 MEDLINE=95327933;
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BAA23674.1;

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D89640;
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                    and sporadic
                       colorectal cancer revealed by immunostaining is based on germline mutations, but rarely on somatic inactivation.",
Int. J. Cancer 97:643-648(2002)
-1- FUNCTION: Restores repair of base-base and single- nucleotide insertion-deletion mismatches, and increases the proficiency t process heteroduplexes with two-, three-, or four- nucleotide insertion-deletion mismatches. GTBP binds covalently to G/T
           of hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
"Involvement of hMSH6 in the development
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P37754;
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                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
SIMILARITY: Contains 1 PWWP domain.
DATABASE: NAME=Hereditary non-polyposis colorectal cancer db;
WWW="http://www.nfdht.nl/".
                                                                                                                                                                                                                                                                                              cities requires a license agreement (send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  U73733; AAB47425.1; JOINED.
U73734; AAB47425.1; JOINED.
U73736; AAB47425.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U73737; AAB47425.1; -.
EMBL; U73732; AAB47425.1; JOINED.
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D89645; BAA23674.1;

EMBL; EMBL; EMBL; EMBL;

SIMILARITY: Belongs to the DNA mismatch repair muts family. SIMILARITY: Contains 1 PWWP domain.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 GSKSK--BAQKGGHFYSAKPEILRAMQRADEALNKDKIKRLELAVCDEPSEPEEEEMEV 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|| :::| ::|| ::|| |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 GDLVWGKLGRYPPWPGKIVNPPKD--LKKPRGKKC-FFVKFF-GTEDHAWIKVEQLKPYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 EEGSSDEISSGVGDSESEGLNSPVKVARKRKRMVTGNGSLKRKSSRKETPSATKQATSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 GTTYVTDKSEEDNEIESEEVQFKTQGSRRSSRQIKKRRVISDSESDIGGSDVEFKPDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 GMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQ-----TEKPAVCYQAITKKLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SOAHVSGGGDDSSRPTVWYHETLEWLK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 ----TDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGR----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --TSSHNSSDDKNRRNSSEERSRPNSGD-----EKRKLSLSEGKVKKNMGEGK---
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28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 1360;
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                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89; Mismatches 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 CEEETGSTSIQAADSTAVN------GSITP---
                                                                                                                                                                                                                                                                                                                                                                                                                                         0.14;
                                                                                                                                                                                                                                                                                                                                                                                         5.2%; Score 148.5;
9.9%; Pred. No. 0.1
BAA23674.1; JOINED.
BAA23674.1; JOINED.
BAA23674.1; JOINED.
BAA23674.1; JOINED.
BAA23674.1; JOINED.
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(Rel. 30, Last sequ
(Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                 19.9%;
                                                                                                                                                                                                                BAA23674.1;
BAA23675.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Escherichia coli.
                                                                                                                                                               D89643;
D89644;
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STRAIN=129/0la;
                                                                                                                  MSH6 OR GIMBP
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                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTFTE-WNEGELSSYLYD-----ITKDIFTKKDEEGKYL-----VDVILDEAANKGTGKW 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQE--GARL--GRTPAEVVST 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GDIIIDGGNTFF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 OQİĞVVGMAVMGRNLALMIESRĞYTVSVENRSREKTEBVIAENPĞKKLVPYYTVQEFVES 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 GEPCVT-----YIGADGAGHYVKNVHNGIEYGDMQLIABAYALLKGGLTLSN--EELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTILDIINQGQLASIFLDQKCQNILQGNF-KPDFYLKYIQKDLRLAIALGDAVNHPT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GLTLAHVTGQSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                  J. Bacteriol. 176:3126-3139 (1994).
-!-CATALVITC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
-:-S-phosphate + CO(2) + NADPH.
-!-PATHWAY: Haxose monophosphate shunt.
-!-PATHWAY: Belongs to the 6-phosphogluconate dehydronenase
                                                                                                            ij
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                          "Cloning and analysis of duplicated rfbM and rfbK genes involved
the formation of GDP-mannose in Escherichia coli 09:K30 and
participation of rfb genes in the synthesis of the group I K30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
                                                                                      Dodgson C., Kido N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.1%; Score 146; DB 1; Length 468; 2.7%; Pred. No. 0.049; ve 51; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREMS, TIGRO0873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP.
SEQUENCE 468 Aa; 51625 MW; C13D94CFD78BFF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 CSSCFQAMGKTSFFLGEVGNAAKWMLIVNMVQGSFMATIAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 EAPVSGNQQLSNDGMLVI---LAAGDRG------
                                                                                   Jayaratne P., Bronner D., Maclachlan R.P., Whitfield C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------PMAAAANEVYKR 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 TSQSSLDLGEPLSLITESVFPR 287
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
InterPro; IPR006114; 6PGD_decarbox.
InterPro; IPR006113; 6PGD_decarbox.
InterPro; IPR006115; 6PGD_NAD.
InterPro; IPR006118; 6PGDOm_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03446; NAD binding_2; 1. PRINTS; PR00076; 6PGDHDRGNASE.
                                                      SEQUENCE FROM N.A.
STRAIN-09:K30:H12 / E69;
MEDLINE-94252978; PubMed=7515042;
                                                                                                                                                                                                                                                                                                                                       EMBL; L27646; AAA21136.1; -.
PIR; I41250; I41250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.1%
Best Local Similarity 22.7%
Matches 73; Conservative
                                                                                                                                                capsular polysaccharide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00393; 6PGD;
                                                                                                                                                                                                                                                                                                                                                                  P00349; 2PGD.
                                NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edelmann W., Yang K., Umar A., Heyer J., Lau K., Fan K., Liedtke W., Cohen P., Kane M.K., Lipford J.R., Yu N., Crouse G.F., Pollard J.W., Kunkel T., Lipkin M., Kolodher R., Kucherlapati R.; "Mutation in the mismatch repair gene Msh6 causes cancer susceptibility.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "CDNA sequence, map, and expression of the murine homolog of GTBP, DNA mismatch repair gene.";
Genomics 36:288-295(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 375-425 AND 1001-1050 FROM N.A.

Donohue P.J., Feng S.L.Y., Alberts G.F., Guo Y., Peifley K.A.,

Hsu D.K.W., Winkles J.A.;

Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: Restores repair of base-base and single- nucleotide

insertion-deletion mismatches, and increases the proficiency to

process heteroduplexes with two., three-, or four- nucleotide

process heteroduplexes with two., three-, or four- nucleotide

insertion-deletion mismatches. GTBP binds covalently to G/T
                                                                                                                                                         (G/T)
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 101 TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Heterodimer of MSH2 and MSH6 (GTBP).
SIMILARITY: Belongs to the DNA mismatch repair mutS family.
SIMILARITY: Contains 1 PWWP domain.
                                                                                   01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA mismatch repair protein MSH6 (MutS-alpha 160 kDa subunit)
mismatch binding protein) (GTBP) (GTMBP) (P160).
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   1358 AA
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      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PWWP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98050922; PubMed=9390556;
InterPro; IPR000432; Muts_C.
InterPro; IPR007860; Muts_III.
InterPro; IPR007896; Muts_III.
InterPro; IPR007891; Muts_IV.
InterPro; IPR007891; Muts_IV.
InterPro; IPR007893; Muts_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U61388; AAB39930.1; -
EMBL; U61389; AAB39931.1; -
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Pfam, PF05188; MutS_II; 1.
Pfam, PF05192; MutS_III; 1.
Pfam, PF05190; MutS_III; 1.
Pfam, PF00488; MutS_IV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U42190; AAC53034.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell 91:467-477(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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EMBL; Y17297; CAA76734.1; -. HSSP; P00349; 2PGD.
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SEQUENCE OF 12-456 FROM N.A.
                                                                                                                                                                                                            Best Local Similarity 22.74
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klebsiella pneumoniae.
                                                                                                                       Pfam; PF00393; 6PGD;
Pfam; PF03446; NAD bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CW 7380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Chedid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6PGD_KLEPN
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                330
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohta M.;
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                                                                                                                                                                                                                                                                                                                                                                                                \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                |||||| |: || || : || || : :|| GDLVWARCHGGYBWWPCLVYNHPFDGTFIRKKGKSVRVHVQFFDDSFTRGWVSKRMLKPYT 152
                                                                                                                                                                                                                                                                                           153 GSKSK--BAQKGGHFYSSKSEILRAMQRADEALSKDTAERLQLAVCDEPSEPEEEBTEV 210
                                                                                                                                                                                                                                                                              ------KGKDQTSS 101
                                                                                                                                                                                                                                                                                                               H----NSSDDKNRRNSSBERSRPNSGDEXRKLSLSEGKVKKNMGEGKKRVSSGSSERGSK 157
                                                                                                                                                                                                                                                                                                                           211 HEAYLSDKSEEDNYNESEEAQPSVQGPRR----SSRQVKKRRVISDSESDIGGSDVEFK 266
                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                   9 GDLVWGKLGRYPPWPGKIVNPPKD--LKKPRGKKC-FFVKFF-GTEDHAWIKVEQLKPYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
6-PGD.
                                                                                                                                                                                                 DB 1; Length 1358;
                                                                                                                           X -> T (IN REF. 2).

X -> D (IN REF. 2).

S -> N (IN REF. 2).

R -> Q (IN REF. 2).

G -> E (IN REF. 2).

W, 2031F78D477804AD CRC64;
                                                                                                                                                                                                                  89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
                                                                                                ATP (POTENTIAL).
DG -> EA (IN REF. 2).
QK -> PE (IN REF. 2).
N -> T (IN REF. 2).
Y -> D (IN REF. 2).
                                                                                                                                                                                                                                                                          65 AHKEEMIKINKGKRFQQAVDAVEEFLRRA-----
                                                                                                                                                                                              5.1%; Score 145.5; DB
24.0%; Pred. No. 0.22;
tive 29; Mismatches
Pfam; PP00855; PWWP; 1.
ProDom; PD001263; MutS_C; 1.
SMART; SM00534; MUTSac; 1.
SWART; SM00533; MUTSd; 1.
SMART; SM00533; PWWP; 1.
PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            485 AA.
                                                                              PWWP.
POLY-GLU.
                                                                  DNA repair; ATP-binding; DNA-binding. DOMAIN 92 154 PWWP.
                                                                                                                                                                                                                                                                                                                                                       SPLKRAQEQSPRKRGRPPKDEKDL 181
                                                                                                                                                                                                                                                                                                                                                                         267 PDTKQEGSSDDASSGVGDSDSBDL 290
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cunninghamellaceae; Cunninghamella
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                                                                                                                                                                   1333 1333
1358 AA; 151075
                                                                                                                                                                                                       Local Similarity 24.09
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                 1139
                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cunninghamella elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4853;
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374
754
800
1227
1329
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                                                                                                                                    CONFLICT
                                                                                                        CONFLICT
                                                                                                                                                       CONFLICT
                                                                                      DOMAIN
NP_BIND
                                                                                                                                                                           SEQUENCE
                                                                                                                             CONFLICT
                                                                                                                                                                                                Query Match
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6PGD_CUNEL
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVSDPKAAKDLVLGPSG-----VLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 RFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTS-----FFLGEVGNA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 LFVGSGVSGGEEGARYGP-SLMPGGNSKAWEHIQPIFQAIAAKAPDGASCCEWVGETGAG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 AKMALLIVNAVQGSFWATIAEGLTLAHV-TGQSQQTLLDIL----NQGQLASIFLDQKCQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genomic organization of the Klebsiella pneumoniae cps region responsible for serotype K2 capsular polysaccharide synthesis in the virulent strain Chedid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DAVNHPTPMAAAANEVYKR 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 LR--FKDTDGQPLVTKIRDTAGQKGTGKWTAIDSLDRGIPVTLIGEAVYSR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P41576; Q48461;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 32, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95204345; PubMed=7896702;
Arakawa Y., Wacharotayankun R., Nagatsuka T., Ito H., Kato N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.0%; Score 143.5; DB 1; Length 22.7%; Pred. No. 0.074; tive 50; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F7E6DDFF3D21EFB2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Pentose shunt; NADP
                                                                                                                                                                                                     InterPro; IPR006183; 6PGD.
InterPro; IPR006114; 6PGD C.
InterPro; IPR006115; 6PGD decarbox.
InterPro; IPR006115; 6PGD MaD.
InterPro; IPR006118; 6PGdom_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 LQGNFKPDFYLKYIQKDLRLAIALG-
                                                                                                                                                                                  InterPro, IPR008927; 6DGDH_C_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95024018; PubMed=7937867;
Nelson K., Selander R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol. 177:1788-1796(1995)
                                                                                                                                                                                                                                                                                                                                                                                                 binding_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS, PRO0076, 6PGDHDRGNASE.
TIGREAMS, TIGRO0873; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 485 AA; 53102 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae; Klebsiella
NCBI_TaxID=573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 KKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDIT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VESLETPRRILLMVKAGAĞTDSAİDSLKPYLDK-------GDIİIDGGNTFFQDTI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 FOAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAE-----GLTLAHVTGQSQQTLL 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VT-----YIGADGAGHYVKMVHNGIEYGDMQLIAEAYALLKGGLALSN--EELAQTFT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 E-WNEGELSSYLID----ITKDIFTKKDEEGKYL----VDVILDEAANKGTGKWTSQS 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 FACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPV
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86;
                                                                                                            PATHWAY: Hexose monophosphate shunt.
SIMILARITY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P00349; 25GD.

R INCEPPRO; IPRO08927; 6DGDH_C_like.

INCEPPRO; IPRO08183; 6PGD_C.

R INCEPPRO; IPRO06118; 6PGD_C.

R INCEPPRO; IPRO06118; 6PGD_C.

R INCEPPRO; IPRO06118; 6PGD_ND.

R INCEPPRO; IPRO06118; 6PGD_ND.

R INCEPPRO; IPRO06184; 6PGD_ND.

R PÉEM; PF00393; 6PGD; 1.

R PÉEM; PF00393; 6PGD; 1.

R PROSITE; PS00076; 6PGDHDRGNASE.

R PROSITE; PS000461; 6PGD; 1.

R QGNOGAG1; 6PGD; 1.

R GLUCONALE Utilization; Oxidoreductase; Pentose shunt; NADP.

CONFLICT 316 316 G-> E (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.9%; Score 141; DB 1; Length 468; 21.4%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 G -> E (IN REF. 2).
121 V -> F (IN REF. 2).
51328 MW, FFIEBSE7665FDC90 CRC64;
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Last annotation update)
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ID _6PGD_SCHPO STANDARD;

AC P78812; Q9UQM5;

DT 15-JUL-1998 (Rel. 36, Created)

DT 16-OCT-2001 (Rel. 40, Last sequ

DT 28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                   EMBL; D21242; BAA04786.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
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Best Local
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Spices of the proposed literate delived communes, decarboxylating (EC 1.1.1.44).

Spices of Schiesascharcovers pome (Frasion year).

Spices of Schiesascharcovers pome (Frasion year).

Schiesascharcovers pome (Frasion year).

Schiesascharcovers pome (Frasion year).

Schiesascharcovers pome (Frasion year).

Spices of Spices (Frasion year).

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                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                              325 DITFACVSDPKAAKDLVLGPSGVLQGIRP----GKCYVDMSTVDADIVTELAQVIVSRGG 380
                                                                                                                                                                                                                                                                                                                                                                          69 KKPRVCILLVKAGKPV----DYLIEGLAPLLEKGDIIVDGGNSHYPDTTRRCEELAKKGI 124
                                                                                                                                                                                                                                                                                                                                                                                                                        RFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTS-----FFLGEVGNA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 AKMMLIVNNVQGSFMATIAE-----GLTLAHVTGQSQQTLLDIL---NQGQLASIFLD 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----EVVSTC 324
                                                                                                                                                                                                                                                                                 10 GLIGLAVMGONLILNGADKGFTVCCYNRTTSRVDEFLANEAK-GKSIVGAHSLEEFVSKL 68
                                                                                                                                                                                              Gaps
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MEDLINE=22272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin O., Yuan E., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Ran B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T.";
                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6-phosphoglucomate dehydrogenase, decarboxylating (BC 1.1.1.44).
GND OR SF2091 OR S2212.
                                                                                                                                        4.8%; Score 138.5; DB 1; Length 492; 22.9%; Pred. No. 0.16; Live 53; Mismatches 127; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=PE577 / Serotype 2a;
MEDLINE=94131953; PubMed=7507920;
Morona R., Mavris M., Fallarino A., Manning P.A.;
"Characterization of the rfc region of Shigella flexneri.";
"J. Bacteriol. 176:733-747(1994).
                                                                                                                                                                                                                                   271 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPA-
                 PROSITE; PS00461; 6PGD; 1.
Oxidoreductase; Pentose shunt; NADP.
CONFLICT 219 220 IA -> ST (IN REF. 1).
SEQUENCE 492 AA; 53679 MW; F55F342957A9D3E1 CRC64;
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STRAIN=2457T / ATCC 700930 / Serotype 2a,
MEDLINE=22590274; PubMed=12704152;
TIGREAMS; TIGRO0873; gnd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae; Shigella
                                                                                                                                                                                     68; Conservative
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                                                                                                                                                               Local Similarity
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P37756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 CDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFL 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 CSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFNATIAE-----GLTLAHVTGQSQ 465
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                                                                                                                       MEDLINE-95024018; PubMed=7937867;
Nelson K., Selander R.K.;
"Intergeneric transfer and recombination of the 6-phosphogluconate dehydrogenase gene (gnd) in enteric bacteria.";
Proc. Natl. Acad. Sci. U.S.A. 91:10227-10231(1994).
-!-CATALYTIC ACITYTITY: 6-phospho-D-gluconate + NADP(+) = D-ribulos
5-phosphate + CO(2) + NADPH.
-!- PATHWAY: Hexose monophosphate shunt.
-!- PATHWAY: Belongs to the 6-phosphogluconate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 4.8%; Score 137; DB 1; Length 468;
l Similarity 20.7%; Pred. No. 0.18;
68; Conservative 54; Mismatches 100; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 AA; 51344 MW; 2203A0D82120CD61 CRC64;
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InterPro; IPR006113; 6PGD decarbox.
InterPro; IPR006115; 6PGD NAD.
InterPro; IPR006184; 6PGdom BS.
Infect. Immun. 71:2775-2786(2003).
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InterPro; IPR006183; 6PGD.
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Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDKGNASE.
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                                                             SEQUENCE OF 12-456 FROM N.A. STRAIN=ATCC 29903;
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BAA15869.1;

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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIKALINE=97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
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corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392(1996).
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                             GPGD_ECOLI STANDARD; PRT; 468 AA.
P00350; P78080;
21-JUL-1986 (Rel. 01, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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Nasoff M.S., Baker H.V. II, Wolf R.B. Jr.;
"DNA sequence of the Escherichia coli gene, gnd, for G-phosphogluconate dehydrogenase.";
Gene 27:253-264(1984).
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SEQUENCE OF 1-125 FROM N.A.
SEQUENCE OF 1-125 FROM N.A.
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MEDLINE-88086897; PubMed=3275621;
Barcak G.J., Wolf R.E. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; K02072; AAA23918.1; -.
EMBL; AE000294; AAC75090.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                          GND OR B2029.
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6PGD ECOLI
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTL----AHVTGQSQQTL 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GDIIIDGGNTFF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 ODTIRRNRELSAEGFNFIGTGVSGGEEGALKGPSIMPGGQKEAYELVAPILTKIAAVAED 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 FTEWNNGELSSYLIDITKDIFTKKDED---GNYLVD------VILDEAANKGT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 QQIGVVGMAVMGRNLALNIESRGYTVSIFNRSREKTEEVIAENPGKKLVPYYTVKEFVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential histone methyltransferase Mes-4 (Maternal-effect sterile 4) MES-4 OR CG4976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 KKIGFLGLGLMGSGIVSNLLKMGHIVTVWNRTAEKCDLFIQE--GARL--GRTPAEVVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 LDILNQGQLASIFLD-----QKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPT
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.7%; Score 136; DB 1; Length 468;
0.0%; Pred. No. 0.21;
ve 54; Mismatches 106; Indels 100;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P -> R (IN REF. 1).
; 62A32C84DC596D86 CRC64;
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 EAPVSGNQQLSNDGMLVI---LAAGDRG---
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Interpro; IPR006113; 6FGD_decarbox.
Interpro; IPR006115; 6FGD NAD.
Interpro; IPR006184; 6FGGOm_BS.
                                                                                                                                                                                                                                                                       InterPro; IPR008927; 6DGDH_C_like.
InterPro; IPR006183; 6PGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00393; 6PGD; 1.
Pfam; PF03446; NAD binding 2; 1.
PRINTS: PR00776; 6PGDHDRGNASE.
TIGREAMS; TIGR00973; gnd; 1.
PROSITE; PS00461; 6PGD; 1.
                                                                                                                                                                                    HSSP; P00349; 2PGD.
ECO2DBASE; C042.6; 6TH EDITION.
EcoGene; EG10411; gnd.
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                         L; M23181; AAA23924.1;
L; M18956; AAA23919.1;
L; M18950; AAA23920.1;
L; M18960; AAA23922.1;
-; D64968; DEECGC.
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CONFLICT 306
SEQUENCE 468 AA;
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                                                                                                                       EMBL;
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Bruton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D.,

Am K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Besson K.Y., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Burkis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

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Cherry J.M., Cawleys J., Dahnes M., Dayan-Rocha S., Plaischmann W.,

R.A. Boodson K., Doup L.E., Downes M., Dayan-Rocha S., Plaischmann W.,

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Alatin D., Hauvey D.A., Hemman T.J., Hernandez J.R., Houck J.,

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Alatin W., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Woly M., Mirphy B., Murphy I., Muzny D.M., Nelson M.S.,

R.A. Beinert K., Remington K., Sunders R.D.C., Scheeler F., Shen H.,

R. Spier E., Spradling A.C., Staplecon M., Skripski M.P., Smith T.,

R. Shins S.M., Wooder T., Worley K.C., Wu D., Yang S., Zhon S.,

R. A., Rom R., Nelson K.A., Worley K.C., Wu D., Yang S., Zhon S.,

R. A., Howlish G.M., Worley K.C., Wu D., Yang S., Zhon S.,

R. A., Romer S.M., Wooley T., Stapler E., Santh T.,

R. A., Mang Z.-Y., Massarmano I.A., Nelnstock G., Wu D., Yang S., Zhon S.,

R. A., Alber R., Myers E.W., Rubinstock G., Wu D., Scheeler F.,

R. A., Myers E.W., Rhon G., Shone M., Shone S., Shone S., Shone S., Shone S., Shone S., Shone S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS
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STRAIN-Berkeley; TISSUE-Embryo;
STRAIN-Berkeley; TISSUE-Embryo;
STRAIN-Berkeley; TISSUE-Embryo;
STRAIN-Berkeley, TISSUE-Embryo;
STRAIN-Berkeley, TISSUE-Embryo;
STRAIN-Berkeley, TISSUE-Embryo;
STRAIN-Berkeley, TISSUE-Embryo;
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P.W., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J.M., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.E.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Potential histone methyltransferase. Histone methylation
gives specific tags for epigenetic transcriptional activation or
repression (By similarity).
-! SUBCELLULAR LOCATION: Nuclear (Probable). "Annotation of the Drosophila melanogaster euchromatic genome: a

Search completed: September 16, 2004, 07:30:47 Job time : 17 secs

-i- SIMILARITY: Contains 3 PHD-type zinc fingers.
-i- SIMILARITY: Contains 1 post-SET domain.
-i- SIMILARITY: Contains 2 PWP domains.
-i- SIMILARITY: Contains 1 SET domains.
-i- CAUTION: Ref.3 sequence differs from that shown due to

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frameshift in position 348.

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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1050 GEIVWAKFNNFRWWPA-IILPPTEVPSNILKKAHGENDFVVRFFGTHDHGWISRRRVYLY 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 GDLVWGKLGRYPPWPGKIVNPPKD----LKKPRGKKCFFVKFFGTEDHAWIKVEQLKPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.7%; Score 135.5; DB 1; Length 1427; 10.7%; Pred. No. 0.98; ve 16; Mismatches 40; Indels 23;
                                                                                                                      R Flybase; FB0003959; Mesa. 1.; Aul_France.
R GO; GO:000028; C:nuclear chromosome; ISS.
R GO; GO:00018959; Fhistone methyltransferase activity; ISS.
GO; GO:0018951; F:histone methyltransferase activity; ISS.
GO; GO:0018952; P:gene silencing; ISS.
R GO; GO:0018952; P:gene silencing; ISS.
R InterPro; IPR004565; AWS.
R InterPro; IPR004514; SET.
R InterPro; IPR001214; SET.
R InterPro; IPR001214; SET.
R EnterPro; IPR001214; SET.
R EnterPro; IPR001265; Znf_PHD.
R Ffam; PF00855; PWWP; 1.
R Pfam; PF00855; SET; 1.
R SMART; SM00570; AWS; 1.
R SMART; SM00293; PWWP; 2.
R SMART; SM00293; PWWP; 2.
R SMART; SM00293; PWWP; 2.
R SMART; SM00293; PWWP; 2.
R PROSITE; PS50864; PWWP; 2.
R PROSITE; PS50868; PWWP; 2.
R PROSITE; PS50868; PWWP; 2.
R PROSITE; PS50868; PWWP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159027 MW; FB6EFD62E814BEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01359; ZF PHD 1; 1.
PROSITE; PSS0016; ZF PHD-2; 1.
Nuclear protein; ZinG-finger; Metal-binding; Repeat.
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PHD-TYPE 1.
PHD-TYPE 2.
PHD-TYPE 3.
                                              entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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                                                                                         EMBL; AE003763; AAF56762.2; -.
EMBL; AY118404; AAM48433.1; ALT_FRANE.
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QBu2w2 pyrococcus
QBa2w4 secherichia
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QB23k1 salmonella
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QBBue9 lactobacill
QB30d1 vibrio vuln
QB9mj7 rhizobium l
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QB9mj8 bordetella
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Score

Result No. salmonella sulfolobus caulobacter

rhizobium m salmonella

Q8xcx6 Q97ze5 Q9c991 Q9ilr8 Q930r8 Q8zzt6 Q974p0

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WEDLINE=21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Azawa T., Hara A., Fukumishi Y., Konoo S., Yamanaka I.,

Salto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov B., Kochiwa H.,

Radota K., Matsudi F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Washimaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashiyaki V.
LTIPESSTVKGMMAGPMAAFKWQPTATEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLK 239
                                                            300
                                                                                                                                                       EKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDM 360
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                                                                                474 FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQS
                                                                                                                                                                                                                                                              STVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Last annotation update)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003693; AAH03693.1; -
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-QCT-2003 (TrEMBLrel. 25, Last annotation update)
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Similar to RIKEN cDNA 3930401K13 gene (Fragment)
                                                                                                                                                                                                                                                                                                                       95.8%; Score 2745.5; DB 96.6%; Pred. No. 2e-184; live 8; Mismatches 4
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InterPro, IPR000313; PWWP_domain. Brain, PR03178; AT hook; 1.
Pfam; PP03446; NND binding_2; 1.
Pfam; PP00855; PWWP; 1.
                                                                                                                                                                                                                                         59744 MW;
                                                                                                                                                           SMART; SM00384; AT hook; 1.
PROSITE; PS50812; PWWP; 1.
SEQUENCE 546 AA; 59744 MV
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   IEA.
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                                                                                                                                                                                                                                                                                                       121 GKVKKNMGEGKKRVSSGSSERGSKSPLKRAQEQSPRKRGRPPKDEKDLTIPESSTVKGMM
                                                                                                                                                                                                                                                                                                                              AGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLKICEBETGSTSIQA
                                                                                                                                                                                                                                                                                                                                                                        ADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARL
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                                                                                                                                                                                                14 GKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHAHKEEMIKI
                                                                                                                                                                                                                   1 GKLGRYPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQLKPYHAHKEEMIKI
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GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; GO; GO:0006098; P:pentose-phosphate shunt; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR006151; 6FGD_NAD.
InterPro; IPR006137; AT_hook.
InterPro; IPR000313; PWWP_domain.
Pfam; PF02178; AT_hook; 1.
Pfam; PF03446; NAD_binding_2; 1.
Pfam; PF00855; PWWP; 1.
                                                                                                                                                                          17;
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BEST:LD22483 OR BEST:LD29743 OR CG4747.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Eddopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                      4; Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEGUENCE FROM N.A.
STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
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                                                                                                                                                                           Indels
                                                                                                                                ED3E2853938A211F CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                   Score 2683.5; DB 4
Pred. No. 4.2e-180;
0; Mismatches 1;
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96.78;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                            PROSITE; PS50812; PWWP; 1.
                                                                                                                                                                  Best Local Similarity 96.7
Matches 522; Conservative
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Connairs M. Chaver C., Dorenter U., Farsin D., Frisa B., George R., Gonnairs M., Charles S., Bronanenavong S., Wan K., Namino J., Pacillo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo J., Pacallo
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EMBL; AB110167; BAC78559.1; -.
GO; GO:0008442; F:3-hydroxytaeobutyrate dehydrogenase activity; IEA.
GO; GO:00004616; F:phosphogluconate dehydrogenase (decarboxyla. .;
GO; GO:0006098; P:pencose-phosphate shunt; IEA.
GO; GO:0006573; P:valine metabolism; IEA.
InterPro; IPR00204; 3hydroxisobut_dh.
InterPro; IPR006183; 6PGD_NAD.
                                            TISSUE=Panicle;
Moriguchi K., Ito Y., Yamazaki Y., Kurata N.;
Moriguchi K. Ito Y. Jamazaki Y., Kurata N.;
Finding of various plant nuclear proteins using yeast nuclear transportation trap system - a proteomal approach.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                  49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289
                                                                                                                                                                                                                                                         Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                      EMBL, AY224558, AAO72678.1, -.
EMBL, AB110167, BAC78559.1, -.
GO, GO:0008442, F:3-hydroxyisol
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                                                                                                                                                                                                                                                                                                                                                                  Similarity
                 [2]
SEQUENCE FROM N.A.
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Q94B07;
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                                                                                                                                                                                                                                                                                                           SERIVGEBATADGNNGVVAHVV--GSPDEGDGLDVEINADSSASPVTSPAVTTKAAGKRT 197
                                                                                                                                                                                                                                                                                                                                                ---KRGRPPKDEKDLTIPESSTVKGMMAGPMAAFKWQPTAS-EPVKDADP 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTC 324
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                                                                                                                                                                                             DLIWAKMKGFTPWPGMIVDPPLDLLSQQRRANTKCVF--FFGSRNFAWIEENNIKPFEGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Nipponbare;
Cooper B., Hutchison D., Park S., Guimil S., Luginbuhl P., Ellero C.,
Goff S., Glazebrook J.,
"Identification of Rice (Oryza sativa) Proteins Linked to the Cyclin-
Mediated Regulation of the Cell Cycle.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Ephratophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                      59;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gamma_hydroxybutyrate dehydrogenase-like protein (Hypothetical
                                                                                                          602;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length
                                                                                                                                    Indels
                                                                        65252 MW; E004EEC610C23625 CRC64;
                                                                                                     Query Match 27.8%; Score 796.5; DB 5; Best Local Similarity 32.8%; Pred. No. 1.8e-47; Matches 192; Conservative 110; Mismatches 225;
                                                                                                                                                                                                                                                                                      L26 KRKLSLSEGKVKKNMGEGKKRVSSGSSERG-----
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              Pfam; PF03446; NAD_binding_2;
Pfam; PF03446; w.c.
Pfam; PF00855; PWWP; 1.
cm00293; PWWP; 1.
                                         SMART, SM00293; PWWP; 1.
PROSITE, PS50812; PWWP;
SEQUENCE 602 AA; 6525
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SEQUENCE FROM N.A
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                                                                                                                                                                                                                 329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS 388
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                                                                                                                                                                                                                                              Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 24, Last annotation update)
Gamma hydroxybutyrate delydrogenase (EC 1.1.1.61).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyra, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Breitkreuz K.E., Van Cauwenberghe O.R., Allen W.L., Jakobs C.,
Talibi D., McLean M.D., Andre B., Shelp B.J.;
"Plant gamma-hydroxybutyrate dehydrogenase, a novel fermentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, ANO441813, AAK94781.1, -.

GO, GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity;

GO, GO:0016491; F:oxidoreductase activity; IEA.

GO, GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla.

GO: GO:00066198; P:pentose-phosphate shunt; IEA.

GO; GO:0006573; P:valine metabolism; IEA.
                                                                                                   ö
                                                             Length 293;
                                                             Score (4),

Pred. No. 5e-43;

...thes 85; Indels
Hypothetical protein. - SEQUENCE 293 AA; 30496 MW; 2362B7AC4EE52038 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVY 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.4%; Score 727; DB 10;
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509
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           Query Match
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                                                                                                                                                                                                               388
                                                                                                                                                                                                                                                                              182 NAFSEGLVLADKSGLSSDTLLDILDLGAMTNPWFKGKGPSMTKSSYPPAFPLKHQQKDMR 241
                                                                                                                                                                                                                                       AMLSDPCAALSVVPDKGGVLEQICEGKGYIDMSTVDAETSLKINEAITGKGGRFVEGPVS 121
                                                                                                                                                                                                                                                                 GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKWMLIVNMVQGSFM 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                 EVGFLGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVEHGASVCESPAEVIKKCKYTI
                                                                                                                                                                                                                329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                  449 ATIAEGLTLAHVIGOSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dehydrogenase-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 3. I. Seque!
features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB025639, BAB01322.1, -.
GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .;
GO; GO:0006099; P:pentose-phosphate shunt; IEA.
GO; GO:0006573; P:valine metabolism; IEA.
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                                                                                                               DB 10; Length 289;
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Te
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
SEQUENCE 289 AA; 30691 MW; 3E67002A19706636 CRC64;
                                                                                        289 AA; 30678 MW; 3E6715DFF96593D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 242 LALALGDENAVSMPVAAAANEAFKKARSLGLGDLDFSAVIEA
                                                                                                                                                                                                                                                                                                                                                                    LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                       93;
                                                                                                              24.3%; Score 697; DB 10;
49.6%; Pred. No. 6.2e-41;
                                                                                                                                        49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006183; 6FGD.
InterPro; IPR006118; 6FGD NAD.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6FGDHDRGNASE.
                                    Pfam, PF03446; NAD_binding_2; 1. PRINE; PRONO76; 6FGDHDRGNASE. PROSITE; PS00895; 3_HYDROXYISOBUT_DH; Oxidoreductase.
InterPro; IPR002204; 3hydroxisobut dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE-20277480; PubMed-10819329;
             InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD_NAD.
                                                                                                                                       Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clones.";
--- pag. 7:131-135(2000)
                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                 389
                                                                                         SEQUENCE
                                                                                                                 Query Match
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                                                                                                                                                                      GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
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                                                                                                                          269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                           Gaps
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   Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
Score 695; DB 10;
Pred. No. 8.6e-41;
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                                 ; Pred. No. 8.6e
49; Mismatches
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      24.28;
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                    49.68;
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Genome Biol. 0:0-0(2002).
                                                                  Matches 140; Conservative
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                                    Best Local Similarity
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Ecker J.R.;
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                           .; IEA
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                                                                                                                                                                                                                  251 IQAADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHIVTVWNRTAEKCDLFIQEG
                                                                                                                                                                                                                                                                                                                     371 LAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEV
                                                                                                                                                                 PMAAFKWQPTASEPVXDADPHFHHFLLSQTEKPAVC----YQAITKKLKICEEETGSTS
                                                                                                                                                                                                                                           -----IGFLGMGIMGSPMAQNLIKAGCDVTVWNRTKSKCDPLVGLG
                                                                                                                                                                                                                                                                                                                                                                                                                       491 QGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Khan S., Brooks S., Buehler B., Chao Q., Johnson-Hopson C., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Chol B., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence for Arabidopsis thaliana BAC F1L3 from chromosome
                          dehydrogenase (decarboxyla. .
                                                                                                                                         38;
                                                                                                                Length 343;
                                                                                                                                        Indels
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                                                                          .l protein.
343 AA; 36287 MW; D012C16284CSFA52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24, Last annotation update)
                                                                                                               23.3%; Score 667; DB 10; 39.4%; Pred. No. 1e-38;
                                                                                                                                        64; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
EMBL; AY085690; AAM62909.1; -.
EMBL; BT008734; AAP42747.1; -.
EMBL; BT008734; AAP42747.1; -.
EMBL; BT008734; AAP42747.1; -.
EMBL; BT008734; Psphosphogluconate dehydrogenase
GO; GO:0006098; Pspentose-phosphate shunt; IEAA
InterPro; IPR006115; 6PGD NAD.
Hypothetical protein.
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01-OCT-2000 (TrEMBLrel. 15, Last seq
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                                                                                                                                         Conservative
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Submitted (APR-2000)
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Submitted (FEB-2000)
                                                                                                                          Similarity
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                                                                                                                                      Matches 142;
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Best Local 2
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                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448
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10 SSSSKAMALCSICPRIPLRFRPKPISP-----FL---SKPQICLAYRVYSSLQS
                                                                                                                                                                                                                                                                                                                                                                                                                          238 KLKICEEFIGSTSIQAADSTAVNGSITPIDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---IGFLGMGIMGSPMAQNLIKAGCDVTVWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --DLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449 ATIABGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΣΗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
AT3925530/MML2 15.
Arabidopsis thaliana (Mouse-ear cress).
Enkaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
NUSI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kamiya D.X., Miranda M., Narusaka P. Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka P. Wayyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai J. Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                  70;
                                                                                                                                                                                                                                                                                DB 10; Length 387;
                                                                                                                                                                                                                                                                                                                                                      186 SSTVKGM---MAGPMAAFKWQPTASEPVKDADPHFHHFULSQTEKPAVC
                                                                                                                                                                                                                                                                            22.5%; Score 644; DB 10; Length 3 36.3%; Pred. No. 5e-37; ive 65; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Arabidopsis cDNA clones.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 RTAEKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAK----
                                                                                                                                                                                                                                            0445432CE8CA0137 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAIALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAVYRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                       Pfam; PF03446; NAD_binding_2; 1.
SEQUENCE 387 AA; 41484 MW; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q94A74;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 TTPSTRDELGTVS---
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                                                                                                                                                                                                                                                                                               Similarity
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-C2A / ATCC 35395 / DSW 2834;

STRAIN-C2A / ATCC 35395 / DSW 2834;

RA Galagan J.E., Nusbaum C., ROY A., Endrizzi M.G., Macdonald P.,

RA EltzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA Lilen N., Navjor J., Strange-Thomann N., DeArellano K., Johnson R.,

Allen N., Navjor J., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Linton L., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., Willer R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Leigh J.A., Li W. Liu J., Mkhopadhyay B., Reeve J.N., Smith K.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic

RI Genome Res. 12:532-542(2002).

BRBL, ABOINT22; AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J. AMMO40581; J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 DITFACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLE 384
                                                                                                                                                                                                                                                      -----DFSSCTVGPMLTRYLFSRLQFQAQKSQQKMGCSSFLP 206
                                                                                                                                                                                                                                                                                                                  425 ---FFLGEVGNAAKMMLIVNNVQGSFMATIAEGLTLAHVTGOSQQTLLDILNQGQLASIF 481
                                                                                                                                                                                                                                                                                                                                                                 LDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSD 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKNITVGVIGLGIMGSSFASNLLSRGYNVHVYNRTKEKAQPLIERGATFHSTPRELASVA 66
KVGFLGLGIMGAPMASNLINAGCDVTVWNRTRSKCDPLLSLGAKYEPSPADVASSCDVTF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 FSLKGPSMVKAAYPTAFPLKHQQKDLRLALALALALASSVSQSIPTVAAANELYKVAKSLGLAD
                                                               329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                           AMLADPESAVEVACGANGAAQGMAPGKGYVDVSTVDAATSKLIGKHITSTGASFLERC--
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Methanosarcinales; Methanosarcinaceae, Methanosarcina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                             389 GNQQLSNDGMLVILAAGDRGLYEDCSSC-
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3-hydroxyisobutyrate dehydrogenase.
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InterPro; IPR006115; 6PGD NAD.
Pfam; PF03446; NAD_binding_2;
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                             GO; GO:0008442; F:3-hydroxylsobutyrate dehydrogenase activity; IEA.
GO; GO:0004616; F:3-hydroxylsobutyrate dehydrogenase (decarboxyla...;
GO; GO:0006039; P:pentose-phosphate shunt; IEA.
GO; GO:0006673; P:pentose-phosphate shunt; IEA.
InterPro; IPR006183; FYGD.
InterPro; IPR006183; GPGD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 248;
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003413; BAB91904.1; -.
                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
SEQUENCE 248 AA; 26336 MW; C96912B3E2A7E677 CRC64;
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Last annotation update)
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51.7%; Pred. No. 1.5e-31;
tive 36; Mismatches 66;
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01-0cT-2002 (TrEMBLrel. 22, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Sasaki T., Matsumoto T.
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Q97XZ7;
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385 APVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQ 444
                                                                                             GSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQ 504
                                                                                                                                                                                    269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQE-GARLGRTPAEVVSTCDIT 327
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PIR; C70303; C70303.
G0; G0:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
G0; G0:0006098; F:pentose-phosphate shunt; IEA.
InterPro; IPR008927; 6DGDH C. like.
InterPro; IPR006115; 6PGD C. like.
InterPro; IPR006115; 6PGD NAD.
Pfam; PF03446; NAD bainding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.7%; Score 392.5; DB 16; Length 31.7%; Pred. No. 1.5e-19; tive 61; Mismatches 132; Indels
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                                                                                                                                                                                                                                                                               247 KDLRLVNEQITKTGAILPMTKVSIEEYSRTVQNGEGQKDFSVI 289
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NCBI_TaxID=63363;
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Best Local Similarity
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SEQUENCE FROM N.A.
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SEOUENCE 288 AA:
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Aquifex aeolicus.
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GO; GO:0008412; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . ; IEA.
GO; GO:0006038; P:pentose-phosphate shunt; IEA.
InterPro; IPR002204; 3hydroxisobut_dh.
InterPro; IPR006183; GPGD.
InterPro; IPR006183; GPGD.
InterPro; IPR006183; GPGD.
InterPro; IPR006184; RNA_rec_mct.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; GPGDHDRGNASE. STRAIN-ATCC 35092 / DSW 1617 / P2;
STRAIN-ATCC 35092 / DSW 1617 / P2;
STRAIN-ATCC 35092 / DSW 1617 / P2;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moores A., Earuso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duquet M., Gaasterland T.,
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The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001). SSO1560. Sulfolobus solfataricus. Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Length 289; Indels 242 YAMEIANSKSLPLIGTSLALQLYNAMVSLGIGELGTQGLVKVY 284 289 AA; 31025 MW; 4EEA33390300E7C7 CRC64; 509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY Last sequence update) Last annotation update) 13.7%; Score 392; DB 17; 29.3%; Pred. No. 1.7e-19; tive 68; Mismatches 132; 289 AA. PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1. PROSITE; PS00030; REM_RNP_1; 1. Created) PRT; EMBL; AE006770; AAK41774.1; -. PIR; G90314; G90314. 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2003 (TrEMBLrel. 25, PRELIMINARY; Conservative

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Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
A yamada K., Sanh J., Banno F., Chang C., Toriumi M., Wu H.C.,
Yamada K., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Kim C., Koesema E., Lam B., Linn J., Meyers M.C., Miranda M.,
A narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
A narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
A Theologis A., Shinozaki K., Davis R.W., Ecker J.R.,
Theologis A., Dana of gene AT4229120 (GI:7269810).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

RMBL, AL161574; CAB796701; -.
BEMBL, AL201971 AX444012.1; -.
BEMBL, AR370197; AAK44012.1; -.
BEMBL, AR370197; AAK44012.1; -.
BEMBL, AR370197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
BEMBL, AR30197; AAK44012.1; -.
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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Variance K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Tang C.C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Full Length CDNA of gene AT4929120 (GI:7269810)."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECULATE FROM N.A.
Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.
Mewes H.W., Lemcke K., Mayer K.F.X.;
e.nhmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                        Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 384; DB 10;
Pred. No. 7.4e-19;
                                                                                              Last sequence update)
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00, 00:0006098; P:pentose-phosphate shunt; IEA.

InterPro; IPR006183; 6PGD.

InterPro; IPR006115; 6PGD_NAD.
                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Last annotation un Hypothetical protein (Putative dehydrogenase) F19B15.150 OR AT4G29120.
              334 AA
                                                                    Created)
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Pfam, PR03446; Mab binding 2; 1.
PRINTS; PR00076; GFQPHDRGNASE.
PROSITE; PS00499; TYROSINASE_2; 1.
                                                                                              (TrEMBLrel. 13,
              PRELIMINARY;
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334 AA; 3
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01-MAY-2000
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Length 334;

13.4%; 32.2%;

Query Match Best Local Similarity

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                                                                                                                                           84 ADSPNSVARQGGVLVDTIVGYPSDVRHVLLDPKSGALSGLRQGGVLVDMTTSEPSLAERIA 143
                                                                                                                                                                                                                                                                                AAKAMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQG 492
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                                   254 ADSTAVNGSITPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARL 313
                                                                                                                  314 GRIPABUVSICDIIFACVSDPKAAKDLVLGP-SGVLQGIRPGKCYVDMSIVDADIVTELA 372
                                                                                                                                                                                                  QVIVSRGGRFLBAPVSGNQQLSNDGMLVILAAGDRGLYBDCSSCFQAMGKTSFFLGEVGN 432
                                                                                                                                                                                                                           GQFAKLANQITIASTWLGLVBGLIYAHKAGLDVKKFLEAISTGAAGSKSIDLYGDRILKR 262
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                                                                                                                                                                                                                                                                                                                                                                                                329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
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                                                                       24 ASSTISSDIITPSNIKIGMIGIGVMGRSMCGHLIKAGYTVTVFNRTISKAQTLIDMGANV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ol-UCI-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Dehydrogenase related to 3-hydroxyisobutyrate dehydrogenase, YKWC
B.subtilis ortholog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. GO; GO:0006098; P:pentose-phosphate shunt; IEA.
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2;
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  Indels
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292 AA; 31542 MW; 7EF0ECC9D59EED87 CRC64;
  152;
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    48; Mismatches
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InterPro; IPR006115; 6PGD_NAD.
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      Conservative
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Best Local Similarity
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Oxidoreductase.
BLR6094.
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01-JUN-2003 (
01-JUN-2003 (
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                              Q89HA0
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127 GGDIGAAEGTLSIMVGGDKEAFDALMPIFELMGKNIVLQGSAGSGQHTKMCNQIAIASNI 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

GO; GO:0008422; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.

GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. .; IEA.

GO; GO:0006573; P:valine metabolism; IEA.

GO; GO:0006573; P:valine metabolism; IEA.

InterPro; IPR00183; 6PGD.

InterPro; IPR006115; 6PGD. NAD.

PRINTS; PR00176; 6PGDHDRGNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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13.0%; Score 373; DB 17; Length 284;
Best Local Similarity 30.2%; Pred. No. 3.5e-18;
Matches 80; Conservative 54; Mismatches 131; Indels (
                                                                                                                                                                               509 LAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00895; 3 HYDROXYISOBUT DH; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 284 AA; 30155 MW; 9D845881717D8550 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
MEDLINE-21664397; PubMed=11792869;
                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoproteaceae; Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein PAE1145.
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=13773;
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01-MAR-2002 (
01-JUN-2003 (
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                                                                                                                                                                                                                                                                                                                   OBZXR3
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RESULT 19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 GQTAKLCNQVIVGCAMAVLAEATRLAVNAGIDANRLPEALAGGFADSIPLQLFVPRMVQG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 QVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGN 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433 AAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDDILNQGQLASIFLDQKCQNILQG 492
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005957; BAC51359.1;
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 NFKPDF-YLKYIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYR 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 IHSPPLGHIATMLKDLDTVADVAQTTSTPVPMATLAGQLFRLAKAARGADADALEIYK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADASKAN---PQRDERFGYLGLGLMGTPMTRRLLKAGYQVSVWNRSEGKVVPIVEAGARH
                                                                                                                                                                                                                                                                                                   MEDLINE=22484998; PubMed=12597275; Raneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabata S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 313;
                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.0%; Score 372.5; DB 16; Length
31.2%; Pred. No. 4.3e-18;
ive 55; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 AA; 32732 MW; 3B92612722105D51 CRC64;
                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                              Created)
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
  PRT;
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PF0716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD_NAD.
                                              24,
24,
25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93; Conservative
                                                                                                                                                                Bradyrhizobium japonicum.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                           (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 SVIPPARNGQLTILVSGEREAFERVRPYLQKLGKRIFYFNEPGKATKLKLINNFVLGAFMA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIAEGLTLAHVTGOSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLRL 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | : | : | : | : | : | | | | | : | 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGWIGLGHIGRAMAERLSE-EYELLVWNRTIEKANGF----KTVARTPEEVAEKCDVIFL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA. GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA. GO; GO:0006098; P:pentose-phosphate shunt; IEA.
                                                                                                                       .; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Bisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Weller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 SLYDSEAVRQV---SERLLSVNLRGKIIVDITINHHEKVLEFHEIYRNVGAFYLESPVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 NOOLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA
                                                                                                                                                                                                                                                                                                                                                             Gaps
STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE010.90; AALBO840.1; -.
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. GO; GO:000608; P:pencose-phosphate shunt; IEA.
InterPro; IPR008927; GDGDL C_like.
InterPro; IPR00812; GDGD NAD.
Pfam; PF03446; NAD_binding_2; 1.
                                                                                                                                                                                                                                                                                                                                                                8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                                                                                                                                                                   Length 278;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAY 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 AYDLAVASRKAVPLNATVRĖIYRLAFEKGLEELDFSVVYRLF 275
                                                                                                                                                                                                                                                                      D755E046098D93B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1-hydroxy-3-oxopropionate reductase.
                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 6.5e-18; 50; Mismatches 133;
                                                                                                                                                                                                                                                                                                                   DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 AA
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InterPro; IPR002204; 3hydroxisobut_dh.
                                                                                                                                                                                                                                                                                                                     12.9%; Score 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015716; AAN55796.1; -.
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MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                      278 AA; 31376 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                              32.3%;
                                                                                                                                                                                                                                                                                                                                                                  91; Conservative
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Shewanella oneidensis.
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                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 278 AA,
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                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                  Matches
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FACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPV 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442 MVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLK 501
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                                                                                                                                                                                                                                                                                                                         269 KIGFLGIGIMGSGIVSNILKMGHTVTVWNRTAEKCDLFIQE-GARLGRIPAEVVSTCDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FICVGNDNDLREVVLGDDGVIHGMALGTVLVDHTTASADVARELHKVLGEKGIDFLDAPV
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EMBL; AP002564; BAB37426.1; -.
PIR; C85974; C85974.
PIR; C91129; C9129.
PIR; JQ0613; JQ0613.
GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
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                                                                                                                                                                                                                                13;
                                                                                                                                                                       DB 16; Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502 YIQKDLRLAIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAV 547
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                                                                                                                                                                                                                                Indels
                                                                                                              31510 MW; 7B7CD7FCA9DB29DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                    ; Score 368.5; DB 16;
; Pred. No. 7.5e-18;
64; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299
InterPro; IPR006115; 6PGD_NAD.
Pfam; PF03446; NAD_binding_2; 1.
PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
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MEDLINE=21156231; PubMed=11258796;
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                                                                                                                                                                             12.9%;
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                                                                                                                                                                                                  30.4%;
                                                                                                                                                                       Query Match
Best Local Similarity 30.4%
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHAE OR Z4477 OR ECS4003.
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Putative dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome seq
0157:H7 and genomic
                                                                                                                       291 AA;
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                                                                                   Complete proteome. SEQUENCE 291 AA:
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InterPro; IPR006115; 6PGD_NAD
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                                                                                                                                                                                                                                                               Local Similarity
nes 80; Conserv
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                                                                                                                                                                                                                                          Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNQQLSNDGMLV1LAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449 ATIAEGLTLAHVIGOSOQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLR 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 AAMSEALTLATKAGVNPDLVYQAIRGGLAGSTVLDAKAPMVMDRNFKPGFRIDLHIKDLA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE008849; AL22120.1; -. GO; GO: 0008679; F:2-hydroxy-3-oxopropionate reductase activity; IEA. GO; GO: 0008442; F:3-hydroxy-3-oxopropionate reductase activity; IEA. GO; GO: 0008442; F:3-hydroxy-isobuty-rate dehydrogenase activity; IEA. GO; GO: 0016491; F: oxidoreductase activity; IEA. GO; GO: 0004616; F: phosphogluconate dehydrogenase (decarboxyla. . .; IEA. GO; GO: 0006593; P: pentose-phosphate shunt; IEA. GO; GO: 0006593; P: valine metabolism; IEA. INTERPRO; IPR002204; 3hydroxisobut_dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAINSIZ / GSGC112 / ATCC 700720;
STRAINSIZ / GSGC112 / ATCC 700720;
MCDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                 5;
GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla., GO:0006098; P:pentose-phosphate shunt; IEA. GO; GO:0006573; P:veline metabolism; IEA. InterPro; IPR002204; Jhydroxisobut_dh. InterPro; IPR005134; Jhydroxisobut_dh. InterPro; IPR006115; 6FGD_NAD. InterPro; IPR006115; 6FGD_NAD. Pfam: PF03446; NAD_binding_2; 1. PFMNFS; PR00076; 6FGDHDRGNASE. TIGRRAMS; TIGR01505; tartro_sem_red; 1. PROSITE; PS000995; JHYDROXYISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                                         12.8%; Score 367; DB 16; Length 299; 29.4%; Pred. No. 9.9e-18; ive 57; Mismatches 140; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509 LAIALGDAVNHPTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: | | : | | : | | 247 NALDTSHGVGAQLPITAAVMEMMQALRADGLGTADHSALACY 288
                                                                                                                                                                                                                                                                                                          299 AA; 31019 MW; 08E65F785BC2B566 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Tartronate semialdehyde reductase (TSAR) (EC 1.1.1.60)
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Salmonella typhimurium.
                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 299 AA;
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 IMLPNSPHVKEVALGENGIIEGAKPGTVLIDMSSIAPLASREISDALKAKGVEMLDAPVS 123
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Nature 423:87-91(2003).

BMBL; AE017011; AAP10951.1; -.

EMBL; AE017011; AAP10951.1; -.

EMBL; AE017011; AAP10951.1; -.

EMBL; AE017011; AAP10951.1; -.

GO; GO:000441; F:0xidoreductase activity; IEA.

GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.

GO; GO:0006098; P:pentose-phosphate shunt; IEA.
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MEDLINE=22608415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Ivanova N., Sorokin A., Anderson I., Galleron N., Lapidus A.,
Kapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Ponstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.,
"Genome sequence of Bacillus cereus and comparative analysis with
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0
                                                                                                                                                                                                                                                                          12.7%; Score 365; DB 16; Length 296; 28.7%; Pred. No. 1.3e-17; tive 59; Mismatches 140; Indels
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Bacteria, Firmicutes, Bacillales; Bacillaceae, Bacillus
InterPro; IPR065398; Tartro sem_red.
Pfam; PP03446; NAD binding 2; 1.
PRINTS; PR00076; GEDHDRGANSE.
TIGRFAMS; TIGR01505; tartro sem_red; 1.
PROSITE; P8008955; 3 HYDROXYISOBUT DH; 1.
Oxidoreductase; Complete protecome.
SEQUENCE 296 AA; 30728 MW; A62B62F3B91F9DFC CRC64;
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SEQUENCE 292 AA; 31987 MW; 8B04FC5E59A93423 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509 LAIALGDAVNHPTPMAAANEVYKRAKALDQSDNDMSAV 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 NALDTSHGVGAQLPLTAAVMEMMQALRADGHGNDDHSAL 282
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31).
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tive 63; Mismatches 144;
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01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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InterPro; IPRO06115; 6PGD NAD.
Pfam; PF03446; NAD binding 2: 1.
PRINTS; PR00076; 6PGDHDRGNASE.
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les 76; Conservative
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PS00895; 3 HYDROXYISOBUT DH; 1.
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PROSITE;
                                                    Query Match
                                                                      Local
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                                                                        68 MYGYPHDVEEVYFGIEGIIEHAKEGTIAIDFTTSTPTLAKRINEVAKRKNIYTLDAPVSG 127
                                                                                                              390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA 449
 270 IGFLGLGLMGSGIVSNILKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFA 329
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STRAIN=TY2 / ATCC 700931;
STRAIN=TY2 / ATCC 700931;
MEDLINE=22231367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                8 IGFIGIGVMGKSMVYHLMQDGHKVYVYNRTKAKTDSLVQDGANWCNTPKELVKQVDIVMT
                                                       CVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSG
                                                                                                                                                                      450 TIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 185:2330-2337(2003).

EMBL; AL627278; CAD07771.1;

EMBL; AL627278; CAD07771.1;

EMBL; ACOUGH 44; ACOUGH 44;

GO; GO: 00008679; F:2-hydroxy-3-oxopropionate reductase activity; IEA.

GO; GO: 00008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.

GO; GO: 0016491; F:oxidoreductase activity; IEA.

GO; GO: 0016491; F:phosphogluconate dehydrogenase (decarboxyla. . .;

GO; GO: 00006098; P:pentose-phosphate shuut; IEA.

GO; GO: 0006573; P:valine metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Bavies R.M., Dowd L., White N., Farrar J., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;
                                                                                                                                                                                                                                            510 AIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRAYI 552
                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEWBLrel. 20, Created)
01-MAR-2002 (TrEWBLrel. 20, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60).
GARR OR STY3430 OR T3168.
                                                                                                                                                                                                                                                                                                                            294 AA
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InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6FGD NAD.
InterPro; IPR006398; Tartro_sem_red.
Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00076; 6PGDHDRGNASE.
TIGRRAMS; TIGR01505; tartro_sem_red; 1.
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                                                                                                                                                                                             269 KIGFLGLGLMGSGIVSNILLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                                                                                                                                                                                             ATIAEGLTLAHVTGQSQQTLLDILNQGQLASIFLDQKCQNILQGGNFKPDFYLKYIQKDLR
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                                                                                                                                       Gaps
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Homson N.R., James K. Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,
Rabbinowitsch E., Saunders D., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Bichner A., Cullum J.,
Kinsshi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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NCBI_TaxID=1902;
                                                                                  Length 294;
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to the EMBL/GenBank/DDBJ databases.
                                                                                                                                       Indels
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                          F2DC91EF41EDEFAE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 NALDISHGVGAQLPLTAAVMEMMQALRADGHGNDDHSAL 280
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Last annotation update)
                                                                            12.6%; Score 361; DB 16; 28.7%; Pred. No. 2.6e-17; iive 58; Mismatches 141;
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Oxidoreductase; Complete proteome
SEQUENCE 294 AA; 30468 MW; F2
                                                                                                                                          80; Conservative
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EMBL; AE015328;
EMBL; AE016989;
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                                                                                                                                                                                         Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                       STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
              "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Infect. Immun. 71:2775-2786(2003).
                                                                                                                                                                 Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                             12.5%; Score 357; DB 16; 32.0%; Pred. No. 4.9e-17; ive 47; Mismatches 137;
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01-JUN-2003 (TrEMBLrel. 24, Last seq
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                          coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                       94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative dehydrogenase.
YHAE OR SF3162 OR S3377
                                                                                                                                                                           Local Similarity
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Hopwood D.A.;
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STRAIN-RB50 / ATCC BAA-588;

MEDLINE-2282954; PubMed=12210271;

MEDLINE-2282954; PubMed=12210271;

RETAIN-RESPERSORY PARCE TO A., Murphy L.D., Thomson N.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Barn N., Cherevach I.,

A Achtman M., Atkin R., Baker S., Basham D., Baron N., Cherevach I.,

A Achtman M., Atkin M., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Reltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Squares R., Squares S., Stevens K.,

Namp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Numin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"Comparative analysis of the genome sequences of Bordetella pertussis,

"The Bordetella parapertussis and Bordetella bronchiseptica.";

BMBL; Bx640449; CAE34588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF 328
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                                 R GO; GO:0008442; F3:1Aydroxyisobutyrate dehydrogenase activity; IEA GO; GO:0008442; F3:1Aydroxyisobutyrate dehydrogenase activity; IEA GO; GO:0004616; F:phosphogluconate dehydrogenase (decarboxyla..., GO; GO:0006573; P:pencose-phosphate shunt; IEA...

R GO; GO:0006573; P:valine metabolism; IEA...

R InterPro; IPR002204; 3hydroxisobut_dh...

R InterPro; IPR006183; GPGD.

R InterPro; IPR006183; GPGD.

R PRINTS; PR000518; GPGD NAD.

R PRINTS; PR00056; GPGDHDRGNĀSE.

R TIGRFAMS; TIGR01505; Lattro_sem_red; 1.

R PROSITE; PS00895; 3_HYDROXYISOBUT_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                  12.5%; Score 357; DB 16; Length 28.7%; Pred. No. 5e-17; cive 57; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509 LAIALGDAVNHPTPMAAAANEVYK--RAKALDQSDNDMSAVY 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 NALDTSHGVGAQLPLTAAVMEMMQALRADGLGTADHSALVCY 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica (Alcaligenes bronchisepticus)
                                                                                                                                                                                                                                                                                                                                                                   299 AA; 30989 MW; 08E65A6C580438A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
AAN44632.1; -. AAP18447.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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GNQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFM 448
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                                                 129 GDIGAESGTLAIMTGGERSVYDYVLPIFQVLGENISYQGPAĞTGQHTKASNQIAIASNMI 188
                                                                                                                                                                                                          189 GVCESLLYAKKAGLDPKKVLATISTGAAASFSLSKLGARMLENDFNPGFYVKHFIKDMRI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 KIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 ACVSDPKAAKDLVLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 GGDLGAKNGTLTIMVGGDQESYDTVLPIFKTFGKTFMLHGSAGKGQHTKMANQLMIAGTM
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390 NQQLSNDGMLVILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22550857; PubMed=12663927;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R., Read T.D., Pouts D.E., Eisen D.A., Gill S.R., Heidelberg J.F., Tettelin H., Doddson R.J., Umayam L., Brinkac L., Beanan M., Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson Wanathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.; "Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0004616; P:phosphogluconate dehydrogenase (decarboxyla. GO; GO:0006098; P:pentose-phosphate shunt; IEA. InterPro; IPR006118; 6PGD. InterPro; IPR006118; 6PGD_NAD. Pfam; PF03446; NAD binding 2; 1. PRINTS; PR00076; 6PGDHDRGNASE.
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                                                                                                                                                                                                                                                                                                                                                                       249 ALESSQAFGLDTPGLKLAIDLYEQLSDMGEQDSGTQALIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Tremblrel. 24, Created)
(Tremblrel. 24, Last sequence update)
(Tremblrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                              510 AIALGDAVNHPTPMAAAANEVYKRAKALDQSDNDMSAVYRA
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llarity 29.9%; Pred. No. 1.5e-16;
Conservative 49; Mismatches 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2-hydroxy-3-oxopropionate reductase.
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Science 299:2071-2074(2003).
EMBL; AE016956; AAO82578.1; -.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
ATCC 700802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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les 79; Conserv
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Q830A7
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                                                                                                                                                                                                                                                                                                                                                          323 TCDITFACVSDPKAAKDLVLGPSGFLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRF
                                                                                                                                                                                                                                                                                                         264 TPTDKKIGFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQE-GARLGRTPAEVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 GAQIVFCCVGNDDDLRSVVLGADGAFAGMQAGAVFVDHTTASADVARELYAAARELNLQF
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Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 30:3927-3935(2002).
Nucleic Acids Res. 30:3927-3935(2002).
BMBL, AP004595; BAC12537.1; -.
GO; GO:0008442; F:3-hydroxyisobutyrate dehydrogenase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006089; P:phosphogluconate dehydrogenase (decarboxyla...;
GO; GO:0006089; P:pentose-phosphate shunt; IEA.
InterPro; IPR006183; 6PGD.
InterPro; IPR006115; 6PGD.NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FYLKYIQKDLRLAIALGDAVNHPT--PMAAAANEVYKRAKALDQSDNDMSAVYR 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
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                                                                                                                                                                                                                               15;
                                                                                                                                                301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oceanobacillus iheyensis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 298;
                                                                                                                                                DB 16; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                               Indels
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                                                             91AC4FBF73F6925F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
3.hydroxyisobutyrate dehydrogenase (EC 1.1.1.31).
0B0581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%; Score 353; DB 16;
27.4%; Pred. No. 9.5e-17;
tive 56; Mismatches 148;
                                                                                                                                            12.4%; Score 354.5; DB 16; 29.6%; Pred. No. 7.6e-17; ive 58; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-HTE831 / DSM 14371 / JCM 11309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03446; NAD binding 2; 1.
PRINTS; PR00176; 6FGDHDRGNASE.
Stridoreductaes; Complete process.
SEQUENCE 298 AA; 31931 MW; 4D
                                                                          31326 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                       87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                              301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=182710;
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                                                                          SEQUENCE
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Soybean 3
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(without alignments)
195.215 Million cell updates/sec
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Aao16415
Aao16415
Aab90720
Aau2160
Abb60930
Abb60930
Abb7422
Abb7422
Aab1422
Aab1922
Aae36392
Aag10424
Aag10424
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Abu17331
Ada36120
Abu17066
Ada36852
Aag10552
Aag10952
Abu29967
Adc95482
Adw27613
                                                                                                                                                                                                                                                                                                            1586107
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                       200
1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                      1586107 seqs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                           protein search, using sw model
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ADC46331
ABB60930
ABM74242
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AAB90720
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AAB19491
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AAE19929
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AAE19927
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ABU24159
ABU17331
ADA36852
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ABU29967
ADC95482
AAW27613
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                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               geneseqp1990s;*
geneseqp200s;*
geneseqp2001s;*
geneseqp2003as;*
geneseqp2003bs;*
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Geneseq 29Jan04:*
1: geneseqp1980s:*
                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
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190 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 227

AAO16415 standard; protein; 553

RESULT 2 AA016415 Human nucleic acid-associated protein (NAAP) - SEQ ID No 12.

(first entry)

10-APR-2003

AA016415;

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The invention relates to human enzyme (ENZM) polypeptides and their corresponding polynucleotides. ENZM sequences are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional ENZM. The disorders include immune disorders (anaemia, allergy or asthma), infectious disorders (arguired immune deficiency syndrome; ALDS), metabolic disorder (Addison's disease, diabetes or goiter), reproductive disorders (Infertility or impotence), cardiovascular disorders (atherosclerosis or myocardial infarction), eye disorders and cell proliferative disorders (cancer). ENZM DNA is useful in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human enzyme (ENZM) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or
Aay99862 Escherich
Add95220 Alcaligen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; enzyme; ENZM; immune disorder; infection; myocardial infarction; gene therapy; anaemia; acquired immune deficiency syndrome; infection; reproductive disorder; cardiovascular; eye; cell proliferation; cancer; AIDS; allergy; asthma; Addison's disease; diabetes; goitre; imporence; infertility; atherosclerosis; metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ring HZ, Lee EA, Forsythe IJ, Khare R;
Richardson TW, Emerling BM, Lindquist EA;
AJA, Jin P, Swarnakar A, Li JX, Marquis JP;
Sprague WW, Becha SD, Elliott VS;
                                                                                                                         ALIGNMENTS
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         AAY99862
ADD95220
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                                                                                                                                                                                                                                                                           AAE38240 standard; protein; 472 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human enzyme (ENZM) protein #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-DEC-2001; 2001US-0340357P.
20-DEC-2001; 2001US-0342962P.
21-DEC-2001; 2001US-0343558P.
22-JAN-2002; 2002US-0351107P.
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Tran UK, Kabi.
Baughn MR, Hafalia P
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Tran UK, Kable AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD57520.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ree SX;
                                                                                                                   Human; nucleic acid-associated protein; NAAP; arteriosclerosis; acell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS; cancer; developmental disorder; renal tubular acidosis; anaemia; asthma; mental retardation; neurological disorder; Alzheimer's disease; epilepsy; Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy; crohn's disease; transgenic animal; animal model.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gandhi AR, Swarnakar A, Hafalia AJA, Warren BA, Emerling BM; Arvizu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forsythe IJ; Ramkumar J, Griffin JA, Yang J, Sanjanwala MM, Baughn MR; Borowsky ML, Yao MG, Walia NK, Bandman O, Lal PG, Becha SD, Richardson TW, Elliott VS, Luo W, Tang YT, Zebarjadian Y, Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid-associated proteins and polynucleotides, useful
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100.0%; Pred. No. 5.2e-20;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 227-228; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-2001; 2001US-0301787P.
29-JUN-2001; 2001US-0301792P.
29-JUN-2001; 2001US-0301892P.
29-JUN-2001; 2001US-0301893P.
06-JUL-2001; 2001US-0303405P.
06-JUL-2001; 2001US-0303442P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-2002; 2002US-0364438P
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nes 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2002;
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                                                                                                                                                                                                                                                                Homo sapiens.
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Length 472; Indels

> 100.0%; Score 200; DB 6; 100.0%; Pred. No. 4.3e-20; Mismatches

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Best Local Similarity 100. Matches 38; Conservative

Query Match

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of diseases associated with inappropriate protein expression. The polypeptides and nucleic acids may be used as nutrients or to modulate cytokine and cell proliferation/differentiation activity and may also be involved in modulation of the immune system. The ORNA sequences, proteins, their agonists and/or antaponists exhibit haematopoiesis regulating activity; tissue growth activity, activin/inhibin activity, receptor/ligand activity, anti-inflammatory activity; and activity; activity, anti-inflammatory activity; and activity anti-inflammatory activity; and activity activity, anti-inflammatory activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAF98490-AAF98572 which are specific for the CDNA clones encoding the secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA clones represented in AAF98374 - AAF98489 encode secreted proteins AAB90667 - AAB90750. The cDNA clones are isolated from various tissue types, and may be used in the prevention, treatment and diagnosis
                                                                              Human, secreted protein; nutrient; cytokine modulator; proliferation;
differentiation; immune system modulator; tissue growth; chemotactic;
haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acids encoding polypeptides, useful for modulating ecytokine and cell proliferation/differentiation activity, the immune system and hematopoiesis regulating activity.
                                           Human AQ73_3 protein sequence SEQ ID 137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 468-470, 557pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU21690 standard; protein; 550 AA.
                                                                                                                                                                                                                                                                                                                 14-SEP-2000; 2000WO-US025135.
                                                                                                                                                                                                                                                                                                                                                          99US-00398829.
  (first entry)
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Treacy M,
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                                                                                                                                                  haematopoiesis.
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Merberg D,
  07-JUN-2001
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KW hype
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                                                                                                                                                                                                                                                                                                                       Secreted protein; nutritional source; cell proliferation activity, cell differentiation activity; immune stimulant; tissue growth activator; haematopoiesis regulator; anti-inflammatory; tumour invasion suppressor; tumour inhibitor; clone AQ73_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is secreted protein, encoded by a polymucleotide of the invention. The DNA was isolated from a human adult ovary cDNA library, and is designated clone AQ73 3. The DNA sequences and encoded polypeptides can be used as mutritional sources or supplements, or may immune stimulating or suppressing activity, haematopoiesis regulating activity, receptor/ligand activity, anti-infilammatory activity, activity, chemostatic/chemokinetic activity, cadherin/inhibin activity, chemostatic/chemokinetic activity, cadherin/tumour invasion suppressor activity, tissue growth activity, tumour inhibition activity or other activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotides - obtained from human adult testis, human adult ovary, human adult brain and human adult heart cDNA libraries.
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                              271 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 308
          GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
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100.0%; Pred. No. 4.3e-15;
live 0; Mismatches 0;
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                                                                                                                                                      AAW69240 standard; protein; 547 AA
                                                                                                                                                                                                                                                                                Clone AQ73_3 protein sequence.
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97US-00989232.
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Spaulding V, Agostino MJ;
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Evans C;

Collins-Racie LA, Evans (Spaulding V, Agostino MJ;

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hyperproliferative disorder; neural disorder; immune system disorder;
muscular disorder; reproductive disorder; gastrointestinal disorder;
                                                                                Gaps
                                                                                0
                           Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human neoplastic disease associated polypeptide #123.
83.0%; Score 166; DB 4; Length 54:
100.0%; Pred. No. 4.3e-15;
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                                                                                                                                                               271 GFLGLGLMGSGIVSNLLKWGHTVTVWNRTAEK 302
                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                               1 Similarity 100.0%; Pred. No. 4.3 32; Conservative 0; Mismatches
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AAB90720 standard; protein; 547 AA.

AAB90720

Best Loc Matches

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AAB90720

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25-SEP-2000; 2000US-023493PP.
26-SEP-2000; 2000US-023493PP.
27-SEP-2000; 2000US-0235834P.
27-SEP-2000; 2000US-0235834P.
27-SEP-2000; 2000US-0235834P.
27-SEP-2000; 2000US-0235836P.
29-SEP-2000; 2000US-0235836P.
29-SEP-2000; 2000US-023637P.
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20-OCT-2000; 2000US-024617P.
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08-DEC-2000;
11-DEC-2000;
       pulmonary disorder; cardiovascular disorder; renal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic.
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01-SEP-2000; 2000US-0229345P.

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29-SEP-2000; 2000US-0236369P.
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07-JUL-2000;
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18-AUG-2000;
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14-SEP-2000;
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       The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA cases are associated polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative cancer, clud and cancer, bladder cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful of the invention may also be useful disorders, muscular disorders, immune system disorders, pulmonary disorders, reproductive disorders, gastrochaftestinal disorders, pulmonary disorders, reproductive disorders and renal clisorders. The polymucleotide sequences of the invention are also useful in gene therapy. AAU21858-AAU21851 represent the novel human neoplastic disease associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                             Novel polypeptides and polynuclectides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neoplastic disease-associated polypeptide, gene therapy, hyperproliferative disease, cancer; autoimmune disorder; diabetes; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder; haematologic disorder; anaemia; thrombocytopaenia; allergic reaction; sthma; cezema; inflammatory disorder; ischaemia-reperfusion injury; inflammatory bowel disease; Crohn's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; renal disorder; acute glomerulonephritis; end-stage renal disease; cardiovascular disorder; atherosclerosis; myocarditis; infectious disease; AlDS; cachexia; anorexia; wound healing; epithelial cell proliferation; Human
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0
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                                                                                                                                                                                      Claim 11; SEQ ID NO 417; 687pp; English.
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                                                            Ruben SM;
05-JAN-2001; 2001US-0259678P.
                            (HUMA-) HUMAN GENOME SCI INC.
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                                                         Barash SC,
                                                                                     WPI; 2001-465558/50.
                                                                                                   N-PSDB; AAS34889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 550 AA;
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Matches 32,
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New isolated human neoplastic disease-associated polypeptides and polymucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's

Claim 11; SEQ ID NO 417; 302pp; English

disease

The invention relates to one of 238 disclosed human neoplastic disease—
associated polypeptides encoded by 171 disclosed cDNA sequences
(including their domains, epitopes, full-length proteins,allelic variants
or specias homologues). Also included are there encoding nucleic acids, a
recombinant vector comprising the nucleic acid, a recombinant host cell
comprising the nucleic acid (expressing the protein), an isolated
antibody that binds specifically to the isolated polypeptide, preventing,
treating or ameliorating a medical condition, diagnosing a pathological
condition or a susceptibility to a pathological condition in a subject,
condition as a susceptibility to a pathological condition in a subject,
condition or a biological assay, and the gene corresponding to the cDNA sequence.
The polypeptides, polynucleotides and antibodies are useful for
detecting, preventing, diagnosing, prognosticating, treating or
cameliorating medical conditions such as hyperproliferative diseases or
cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
contended anneamia) haematopoietic or haematological confers (e.g.
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Gaps

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Length 550; Indels

83.0%; Score 166; DB 7; L 100.0%; Pred. No. 4.3e-15; iive 0; Mismatches 0;

Best Local Similarity 100. Matches 32; Conservative

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Query Match

anaemia or thrombocytopaenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,

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2000US-0249211P.
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N-PSDB; ADC46047.
                              02-OCT-2000; 2
02-OCT-2000; 2
13-OCT-2000; 2
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20-OCT-2000; 2
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                          Drosophila, developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 9582; 21pp + Sequence Listing; English.
                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 9582.
                                                                                                                                                                                                                                                                                               Myers EW;
                     ABB60930 standard; protein; 574 AA
                                                                                                                                                                                                                                                                                               Li PWD,
                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
                                                                 (first entry)
                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                Venter JC, Adams M,
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                                                                                                                           pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                               interactions.
                                                                                                                                                                                              27-SEP-2001.
                                                                 26-MAR-2002
                                             ABB60930;
RESULT 7
ABB60930
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            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Darley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fit, wipo.int/pub/published-pct-sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention relates to oligonucleotide clones originating in
                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA clone originating in barley containing SNP sequence #652.
                                                                                                                                                                                                                                      63.0%; Score 126; DB 4; Length 574; 60.5%; Pred. No. 2.8e-09; Live 5; Mismatches 10; Indels
                                                                                                                                                                 from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                           291 GFLGLGMMGSTIVKDLIYTGHKVVVWNRTIDKCQPFAE 328
                                                                                                                                                                                                                                                                                                     1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID XX; 284pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                        ABM74242 standard; protein; 161 AA.
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2001JP-00403299.
2001JP-00403300.
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                                     Gaps
                                     ..
                  Length 161;
                62.5%; Score 125; DB 7; Length 16
64.7%; Pred. No. 8.1e-10;
ive 5; Mismatches 7; Indels
                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 51261.
                                                 1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                            48 GFLGLGIMGAPMASNLIKAGCDITVWNRTKSKCD 81
                                                                                                            AAG41222 standard; protein; 168 AA.
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9903-0130077P.
9903-0130449P.
9903-0130510P.
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99US-0127462P.
99US-0128234P.
99US-0128714P.
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                        Local Similarity 64.7
les 22; Conservative
                                                                                                                                                                                                                   Arabidopsis thaliana.
Sequence 161 AA;
                                                                                                                                                                                                                                                                                                                                                 06-APR-1999;
08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
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AUG-1999; 9 AUG-1999; 9 AUG-1999; 9 AUG-1999; 9 AUG-1999; 9 AUG-1999; 9 AUG-1999; 9 AUG-1999; 9 AUG-1999; 9 AUG-1999; 9 AUG-1999; 9 AUG-1999; 9 AUG-1999; 9 AUG-1999; 9	400 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
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Query Match 62.5%; Score 125; DB 3; Length 168; Best Local Similarity 60.5%; Pred. No. 8.5e-10; Matches 23; Conservative 4; Mismatches 11; Indels

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Novel isolated nucleic acid fragment encoding a tuliposide A synthesizing protein, useful for creating recombinant organisms that have the ability to synthesize tulipalin A, tuliposide A or tuliposide A pathway
                                                              enzyme; gamma-aminobutyrate aminotransferase; UDP-glucosyltransferase; gamma-hydroxybutyrate dehydrogenase; tulipalin A; plant; mouse-ear cress.
                                               Alpha-methylene-gamma-butyrolactone; glutamate decarboxylase; herbicide;

    A. thaliana gamma-hydroxybutyrate dehydrogenase homologue.

                                                                                                                                                                                                                                                                                                                                                                                                             Claim 22; Page 112-113; 71pp; English
                                                                                                                                                                                                                                     (DUPO ) DU PONT DE NEMOURS & CO (PRAB/) PRABHU V.
                                                                                                                                                                                 10-JUN-2002; 2002WO-US018230.
                                                                                                                                                                                                            08-JUN-2001; 2001US-0297198P.
                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                            Damude HG, Flint D,
                                                                                                                                                                                                                                                                                                     WPI; 2003-201331/19
                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD55025
                                                                                                                              WO2002101013-A2
                                                                                                                                                                                                                                                                                                                                                                                    intermediates.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel proteins related to gamma aminobutyric acid (GABA) metabolism, GABA-transaminase and gamma hydroxy butyrate dehydrogenase useful for screening and isolation of homologous genes from other organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a plant gamma-hydroxy butyrate dehydrogenase (GHBDH). The specification also describes a plant gamma-aminobutyric acid (GABA) transaminase (GABA-T). The proteins are involved in the metabolism of GABA in plants. GABA-T is used to transaminate GABA to form succinic semialdehyde, which may be converted to gamma hydroxybutyrate by GHBDH. The polynucleotides are used to produce GABA-T and CHBDH recombinantly. The proteins are useful for screening and isolation of homologous genes from other organisms
                                                                                                                                                                                                                                                                                                         /note= "these residues are encoded by nucleotides 1-300"
                                                                                                                                                                      Amino acid sequence of gamma-hydroxy butyrate dehydrogenase (GHBDH)
                                                                                                                                                                                                 Gamma-aminobutyric acid; GABA; GABA transaminase; GABA-T;
gamma-hydroxy butyrate dehydrogenase; GHBDH; succinic semialdehyde;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 289;
 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                      4 GFLGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Cauwenberghe OR;
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Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                          AAB19491 standard; protein; 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Fig 5; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2000; 2000WO-CA000378.
                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0128518P
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                                                                                                                                             (first entry)
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                                                                                                                                                                                                                            gamma hydroxybutyrate.
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                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-679492/66.
N-PSDB; AAC62027.
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                                                                                                                    AAB19491;
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Ξ, Wang

Prabhu V,

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The invention relates to genes encoding key enzymes in the biosynthesis of alpha-methylene-gamma-butyrolactone (tulipalin A). Key enzymes include glutamate decarboxylase, gamma-aminobutyrate aminotransferase, gamma-hydroxybutyrate dehydrocognase and UDP-glucosyltransferase. The invention is useful for producing tulipalin A or tuliposide A or its pathway intermediates such as alpha-methylenesuccinate semialdehyde, alpha-
                                                                                                                                                 methylene-gamma-aminobutyrate or alpha-methylene-gamma-hydroxybutyrate. Tulipalin A sequences are used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for them or as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. The present sequence is mouse-ear cress (Arabidopsis thaliana) gamma-hydroxybutyrate dehydrogenase homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Branched chain amino acid degradation enzyme; HMG-COA lyase;
3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl COA;
isovaleryl-COA dehydrogenase; transgenic plant; soybean; EC 1.1.131.
                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                     Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFLGLGIMGKAMSMNLLKNGFKVTVWNRTLSKCDELVE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ
                                                                                                                                                                                                                                                                                                                                                                                Score 125; DB 6;
Pred. No. 1.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              23; Conservative
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AAE36392 standard; protein; 289 AA

RESULT 11

AAE36392

(first entry)

26-JUN-2003

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1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ

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9905-0142154P-
9905-014230P-
9905-014230P-
9905-0142920P-
9905-014294P-
9905-0143624P-
9905-0143624P-
9905-0144065P-
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990S-013423P.
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13-JUL-1999;
14-JUL-1999;
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04-MAY-1999;
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21-MAY-1999;
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                                                                                                                                                                                        The invention relates to nucleic acid fragments encoding branched chain amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutyrate dehydrogenase, 3-hydroxymethylgulutary! CoA (HMG-CoA) lyase and isovalery!-CoA dehydrogenase polypeptides and polynucleotides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. Polynucleotides of the invention can be used as probes for physical mapping of genomes. The present sequence is soybean 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) from ses2w.pk0002.e5 clone
                                                                                                                                         Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase, used to produce transgenic plants having an altered expression of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                 62.0%; Score 124; DB 5; Length 345; 64.9%; Pred. No. 2.9e-09;
                                                                                                                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 8740.
                                                                                                                                                                                                                                                                                                                                                         1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                    Rafalski JA;
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                                                                        (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAG10424 standard; protein; 343 AA
                                                                                                                                                                          Claim 1; Col 33-36; 40pp; English
                                                                                             Kinney AJ,
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99US-0123180P.
99US-012548P.
99US-0126788P.
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                                                      98US-0094990P.
                                 99US-00364230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                    Query Match 62.0
Best Local Similarity 64.9
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                             Cahoon RE, Hitz WD,
                                                                                                               WPI; 2002-204621/26
                                                                                                                          N-PSDB; AAD31750
                                                                                                                                                                                                                                                                                                 Sequence 345 AA;
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24-SEP-1999
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                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                     61.5%; Score 123; DB 3; Length 343; 64.7%; Pred. No. 4e-09;
                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 8739.
                                                                                                                                                                                                                                                     1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                   AAG10423 standard; protein; 353 AA.
        990S-0159637P

990S-0159638P

990S-0160767P

990S-0160768P

990S-0160768P

990S-0160814P

990S-0160815P

990S-016089P

990S-016089P

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                                                                                                                                                                                                                                                                                                                                                        (first entry)
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es 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
14-OCT-1999;
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The invention relates to nucleic acid fragments encoding branched chain amino acid degradation enzymes. Particularly the invention relates to 3-hydroxyisobutyrate dehydrogenase, 3-hydroxymethylgiutaryl CoA (HMG-CoA) lyase and isovaleryl-CoA dehydrogenase polypeptides and polynucleotides derived from corn, rice and wheat. Sequences of the invention are used to produce transgenic plants having an altered expression of the enzyme. Polynucleotides of the invention can be used as probes for physical mapping of genomes. The present sequence is corn 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) from crln.pk0191.bl0, p0076.cwhan08r and
                or monoclonal antibodies with specificity for them or as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. The present sequence is Tulip pistil gamma-hydroxybutyrate dehydrogenase homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              produce transgenic plants having an altered expression of the enzyme.
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polynucleotide encoding 3-hydroxyisobutyrate dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Branched chain amino acid degradation enzyme; HMG-CoA lyase;
3-hydroxyisobutyrate dehydrogenase; 3-hydroxymethylglutaryl CoA;
isovaleryl-CoA dehydrogenase; transgenic plant; corn; EC 1.1.131.
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                                                                                                                                                                                                                  Length 290;
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                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                      1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFIQ 38
                                                                                                                                                                                                                                                                                                                                                                      41
                                                                                                                                                                                                                                                                                                                                         Score 118, DB 6,
Pred. No. 1.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
B
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Pred. No. 3.1e-08;
4; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 GFLGLGIMGKAMATNLLRHGFRVTVWNRTLAKC 101
                                                                                                                                                                                       59.0%; Sco...
55.3%; Pred. No. ....
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corn 3-hydroxyisobutyrate dehydrogenase #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE19927 standard; protein; 360 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinney AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00364230.
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Best Local Similarity 63.69
....hes 21; Conservative
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                                                                                                                                                                                                                             Similarity
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                                                                                                                                                 Sequence 290 AA;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid fragment encoding a tuliposide A synthesizing protein, useful for creating recombinant organisms that have the ability to synthesize tulipalin A, tuliposide A or tuliposide A pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to genes encoding key enzymes in the biosynthesis of alpha-methylene-gamma-butyrolactone (tulipalin A). Key enzymes include glutamate decarboxylase, gamma-aminobutyrate aminotransferase, gamma-hydroxybutyrate dehydrogense and UDP-glucosyltransferase. The invention is useful for producing tulipalin A or tuliposide A or its pathway intermediates such as alpha-methylenesuccinate semialdehyde, alphamethylene-gamma-hydroxybutyrate. Tulipalin A sequences are used to immunise animals to produce polyclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-methylene-gamma-butyrolactone; glutamate decarboxylase; herbicide;
enzyme; gamma-aminobutyrate aminotransferase; UDP-glucosyltransferase;
gamma-hydroxybutyrate dehydrogenase; tulipalin A; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 123; DB 3; Length 353;
Pred. No. 4.1e-09;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tulip pistil gamma-hydroxybutyrate dehydrogenase homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GFLGLGLMGSGIVSNLLKWGHTVTVWNRTAEKCD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFLGMGIMGSPMAQNLIKAGCDVTVWNRTKSKCD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 110-111; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE36391 standard; protein; 290 AA
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                                           99US-0160815P.
99US-0160980P.
99US-0160981P.
99US-0160989P.
99US-0161404P.
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99US-0161359P.
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99US-0160770P
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                                                                                                                                                                                                                                                                                                                                                                                                                                            61.5%;
64.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-2002; 2002WO-US018230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                    25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
                                                                                                                                                                                                                                                                                                      28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                21-0CT-1999
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                                                                      22-OCT-1999
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25-0CT-1
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AAE36391

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Sequence 292 AA;

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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibitiang cellular proliferation or the activity of a gene in an operon required for proliferation or that inhibits cellular required for proliferation, (7) identifying a compound that influences the activity of dentifying a gene required for cellular proliferation or the the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound; a activity; (11) a culture comprising strains in which the gene product is overexpressed; (12) identifying the target of a compound that inhibits the credit of the strains; or (13) identifying the target of a compound that inhibits the credit of confidentifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, crediting proteins or screening pences and cell acids required for proliferation in cells other than S. aureus, S. typhimurium, credit and antibior provint obsential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at credit and control of control of control of cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one of
                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen KL,
Forsyth RA,
                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #9686.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID NO 52083; 1766pp; English.
                                        ABU24159 standard; protein; 292 AA
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                   Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC.
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Trawick JD,
                                                                                                                                        (first
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N-PSDB; ACA28029
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08-FEB-2002;
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                                                                                             ABU24159;
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Wall |
RESULT 17
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: of the nucleic acid inhibits proliferation of a cell. Also included are: coding a polypeptide whose expression is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated on polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding collypeptide; (5) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway in which the test compound that influences the product lies or a gene on which the test compound the inhibits proliferation or the biological corpanism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound the train in a culture or collection of the which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind JW;
Xu HH;
                                                           Gaps
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Length 292
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Yamamoto R, Forsyth RA,
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #2858.
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9
Score 109; DB 6;
Pred. No. 3.4e-07;
                                                                                                                         1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTABK 32
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                                                                 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      ABU17331 standard; protein; 288
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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   54.5%;
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                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acinetobacter baumannii.
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Trawick JD,
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                                    Local Similarity
nes 20; Conserv
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Wall D,
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         Query Match
                                                                        Matches
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GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD

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identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumanni and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                          53.0%; Score 106; DB 6; Length 288; 55.6%; Pred. No. 9.2e-07;
                                                                                                                                                                                                                                             11; Indels
                                                                                                                                                                                                                                                                           2 FLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                               Pred. No. 9.2e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acinetobacter baumannii protein #3281.
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                                                                                                                                                                                                                                                                                                                                                                                            ADA36120 standard; protein; 299
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                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acinetobacter baumannii plant biocontrol agent.
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                                                                                                                                                                                                                        Best_Local Similarity
Matches 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Breton G, Bush D;
                                                                                                                                                                         Sequence 288 AA;
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                                                                                                                                                                                                        Query Match
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21-MAR-2001; 2001US-00815542. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851.

21-MAR-2002; 2002WO-US009107.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Acinetobacter baumannii.

WO200277183-A2

03-OCT-2002

Protein encoded by Prokaryotic essential gene #2593

(first entry)

19-JUN-2003

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ABU17066;

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ABU17066 standard; protein; 290

RESULT

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the invention traters to an increase acts comparisons only the invention traters to an increase acts and the facts and antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: concluded a procession is inhibited by the antisense ancience and search (2) a host cell containing the vector; (3) an isolated concluded antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding can the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular continguation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway in the gene product or that has an activity against a biological pathway in definition or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product its compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of the wind that inhibits and the form of the provint of an overanism of the arrains is present in a culture or collection of an overanism. The antisoned minimises the province of an operon required for product is overexpressed or underexpressed. (2) determining the extent of a compound in the inhibits and province of a compound in the inhibits and province of a compound in the inhibits and province of an entire or collection of an extension of an extension of an extension of an extension of an extension of an extension of an extension of an extension of an extension of an extension of an extension of an extension of an extension of an extens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   required for proliferation in cells other than S. aureus, S. typhimurium,
K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 44990; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-029926/02
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Wall D,
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; 0

Gaps

0;

10; Indels

6; Mismatches

Conservative

Query Match Best Local Similarity Matches 18; Conserv

baumannii protein.

Sequence 299 AA;

53.0%; Score 106; DB 6; Length 299; 52.9%; Pred. No. 9.6e-07;

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10-JUN-1999;
10-JUN-1999;
14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
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30-APR-1999;
04-MAY-1999;
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19-MAY-1999;
20-MAY-1999;
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07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAY-1999;
11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1999;
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14-MAY-1999;
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27-MAY-1999;
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                                                                                                                                                                                          06-SEP-2000.
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05-MAR-1999;
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09-MAR-1999;
                                                                                                                                                                                                                                                                                            01-APR-1999
                                                                                                                                                                                                                                                                                 29-MAR-1999
                                                                    17-0CT-2000
                                                                                                                                                                                                                                                              23-MAR-1999
                                                AAG10425;
          RESULT 22
                     AAG10425
                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial Accines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                           Gaps
                                                                                                                                                                                                                                                                 baumannii; bacterial disease; antibacterial; vaccine;
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0
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                                                                       Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                           Indels
                                                                  Score 105; DB 6; Le
Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 FLGIGLMGSRMASRLIQAGFQVAVWNRTTSACEELI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                 GFVGTGIMGMPMAMNLLKAGHOVKVWNRTSSK 36
                                                                                                               1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; SEQ ID NO 8139; 328pp; English.
                                                                                                                                                                                                                                               Acinetobacter baumannii protein #4013.
                                                                                                                                                                                     ADA36852 standard; protein; 326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.0%;
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                                                                                                                                                                                                                                                                                                                                                                                 98US-0088701P
                                                                        52.5%;
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                                                                                               Conservative
                                                                                                                                                                                                                                                                                                  Acinetobacter baumannii.
                                                                                                                                                                                                                                                                               plant biocontrol agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 19; Conserv
                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        Bush D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 326 AA;
                                                      Sequence 290 AA;
                                                                                                                                                                                                                                                                     Acinetobacter
                                                                                                                                                                                                                                                                                                                                                             04-JUN-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 8741.
AAG10425 standard; protein; 285 AA.
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9905-0132485F.
9905-0132487F.
9905-0132487F.
9905-0134256F.
9905-0134256F.
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990S-0134221P.
990S-0134770P.
990S-0134768P.
990S-0134941P.
990S-0135353P.
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99US-0139455P.
99US-0139456P.
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99US-0123180P.
99US-0125788P.
99US-0126788P.
99US-0126785P.
99US-0127482P.
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99US-0136021P.
99US-0136392P.
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99US-0137222P.
99US-0137528P.
99US-0137502P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0131449P.
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                                                          (first entry)
                                                                                                                                                    termination sequence
                                                                                                                                                                                Arabidopsis thaliana
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PR 18-70N-1999; 95078-0139458P
PR 18-70N-1999; 95078-0139458P
PR 18-70N-1999; 95078-0139462P
PR 18-70N-1999; 95078-0139462P
PR 18-70N-1999; 95078-0139462P
PR 18-70N-1999; 95078-0139462P
PR 28-70N-1999; 95078-0139462P
PR 28-70N-1999; 95078-0139462P
PR 28-70N-1999; 95078-0139492P
PR 28-70N-1999; 95078-013993P
PR 28-70N-1999; 95078-013993P
PR 28-70N-1999; 95078-013993P
PR 28-70N-1999; 95078-013993P
PR 28-70N-1999; 95078-013993P
PR 18-70N-1999; 95078-013993P
PR 18-70N-1999; 95078-013494P
PR 18-70N-1999; 95078-013494P
PR 18-70N-1999; 95078-013494P
PR 18-70N-1999; 95078-013494P
PR 18-70N-1999; 95078-013494P
PR 18-70N-1999; 95078-013494P
PR 18-70N-1999; 95078-013494P
PR 18-70N-1999; 95078-013494P
PR 18-70N-1999; 95078-013494P
PR 18-70N-1999; 95078-013494P
PR 28-70N-1999; 95078-01349
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Gaps
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60.0%; Pred. No. 4.8e-06;
iive 4; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 23
ABU29967
ID ABU29967 standard; protein; 295 AA.
XX
AC ABU29967;
990S-0149723P.
990S-0149922P.
990S-0149930P.
990S-015084P.
990S-0151084P.
990S-0151080P.
990S-0151080P.
990S-0151303P.
990S-0153130P.
990S-015313P.
990S-015313P.
990S-015313P.
990S-015403P.
990S-015403P.
990S-015403P.
990S-015596P.
990S-015536P.
990S-015536P.
990S-015536P.
990S-015536P.
990S-015536P.
990S-015536P.
990S-015536P.
990S-015659F.
990S-015659F.
990S-015659F.
990S-015659F.
990S-015659F.
990S-015963P.
990S-015963P.
990S-015963P.
990S-015963P.
990S-015963P.
990S-015963P.
990S-016968P.
990S-016074P.
990S-016098P.
990S-016098P.
990S-016098P.
990S-016136P.
990S-016098P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
01-SEP-1999;
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05-0CT-1999;
06-0CT-1999;
07-0CT-1999;
                                                                                                                                                                                                                                                                 18-0CT-1999
21-0CT-1999
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25-0CT-1999
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28-0CT-1999
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Matches
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Enterococcus faecium.
                                              2003-029926/02
                                                                                                                         Sequence 295 AA;
                                               N-PSDB; ACA33837
              WO200277183-A2.
                         21-MAR-2001;
19-JUN-2003
                  03-OCT-2002
                                        Wang L,
Wall D,
                                              WPI;
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Enterococcus facetium encoding an Enterococcus facetium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 one of 10 fully defined sequences given in the (or comprising 40 one of 10 fully defined sequences given in the (or comprising 40 one of 10 fully defined sequences from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a crecombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-extranded probe comprising the nucleic acid. The nucleic acids are chosen from 364 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions cresulting from E. facetium bacterial infection (e.g. urinary tract infection) bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaccutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid derived from Enterococcus faecium encoding
                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine, urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 50.0%; Score 100; DB 7; Similarity 52.9%; Pred. No. 7.1e-06; 18; Conservative 6; Mismatches 10;
4 GFIGTGVMGSAVARHLLEAGHEVAVYNRTKAKAD 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 5109; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the disclosed E. faecium proteins
                                                                                                                                                                                                                                                                                                                                                                     E. faecium protein sequence SEQ ID 5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                       ADC95482 standard; protein; 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0051571P.
98US-0085598P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADC91828.
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                                                                                                                                                                                                                                                      ADC95482;
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                                                                                                                                    RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the 6213 antisense sequences given in the specification where expression of the muchaic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated nucleic acid; (2) a host cell containing the vector; (3) an isolated or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation required gene or its gene product lies to a gene or which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of the which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the contribution or an organism. The antisense nucleic acids are useful for an admitishing the extent contribution or an organism. The answer maniform and antibiodical acids are useful for a definition or an organism. The antisense nucleic acids are useful for an admitishing the extent contribution or an organism. The antisense nucleic acids are useful for a definition or an encodic are useful for a definition or an encodic are useful for a definition or an organism. The encode of an encode are useful for a definity and antibion or an encode are useful for a definition or an en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
                                                                           Protein encoded by Prokaryotic essential gene #15494.
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Yamamoto R,
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Carr GJ,
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25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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Gaps

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Length 299; Indels

Query Match Best Local Similarity

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Matches

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99US-0126264P.
99US-0126785P.
99US-0126782P.
99US-0128714P.
99US-0130845P.
99US-0130845P.
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9905-0131449P.
9905-0132484P.
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9905-0134218P.
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14-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                             6-phospho:gluconate dehydrogenase - can be recombinantly produced by transforming coryneform bacteria with DNA molecule encoding it.
                                                                                                                                                                                                                                                                                         The present sequence is the Brevibacterium flavum JM-233 6-phosphogluconate dehydrogenase (6-PD). The 6-PD can be recombinantly produced by transforming coryneform bacteria with the DNA molecule encoding it
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                                                                               Brevibacterium flavum; 6-phosphogluconate dehydrogenase; recombinant production; coryneform; bacterium; bacteria.
                                                             Brevibacterium flavum 6-phosphogluconate dehydrogenase.
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                                                                                                                                                                                                                                                                                                                                                                                          1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                                                                                      AAW27613 standard, protein, 492 AA.
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                                                                                                                                                                                                                                                                       Claim 1; Page 5-7; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0121825P.
99US-0123180P.
99US-0123548P.
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                                            22-DEC-1997 (first entry)
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Best Local Similarity 45.99
Matches 17; Conservative
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                                                                                                          Brevibacterium flavum
                                                                                                                                                                                                                   WPI; 1997-484097/45.
N-PSDB; AAT88035.
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05-MAR-1999;
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AAG06417
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99US-0144085P.
99US-0144285P.
99US-0144331P.
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99US-0144332P.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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Pred. No. 4.7e-05;
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                                                                                                                                                                                                                                                                                                                               1 GFLGLGLMGSGIVSNLLKMGHTVTVWNRTAEKCDLFI 37
                                                                                                                                                                                                                                                                                                                                           19 GWIGTGVMGRSMCGHLIKAGYTVTVENRTISKAQTLI
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99US-0123180P.
99US-012548P.
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99US-0128234P.
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09-MAR-1999;
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45.9%; Pred. No. 5.5e-05;
ive 8; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                               Length 182;
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